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OM protein - protein search, using sw model

Run on: December 23, 2004, 18:30:04 ; Search time 155.692 Seconds
(without alignments)
1340.986 Million cell updates/sec

Title: US-10-089-500-53
Perfect score: 3071
Sequence: 1 EVQLVESGGDFVQPGGSLRV.....IVEFLNRWITFCQSIISTLT 582

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3071	100.0	582	4	AAB81987	Aab81987 Gangliosi
2	3026	98.5	582	4	AAB81991	Aab81991 Gangliosi
3	2780.5	90.5	583	4	AAB83156	Aab83156 Gangliosi
4	2760.5	89.9	581	4	AAB81972	Aab81972 Gangliosi
5	2750.5	89.6	579	6	AAE33444	Aae33444 KS antibo
6	2750.5	89.6	579	6	AAO30910	Aao30910 dI-KS-ala
7	2719.5	88.6	575	8	ADP42961	Adp42961 Humanised
8	2621	85.3	580	6	AAO30915	Aao30915 dI-NHS76
9	2589	84.3	580	6	AAO30913	Aao30913 dI-NHS76
10	2246.5	73.2	447	6	AAE33522	Aae33522 Human AQC
11	2240.5	73.0	447	6	AAE33523	Aae33523 Human AQC
12	2238.5	72.9	449	5	AAO18400	Aao18400 Mature hu
13	2236.5	72.8	447	6	AAE33524	Aae33524 Human AQC
14	2236.5	72.8	450	8	ADH34587	Adh34587 023 heavy
15	2234.5	72.8	445	6	AAO31101	Aao31101 Human A2-
16	2233	72.7	449	6	ABP58273	Abp58273 Humanised
17	2233	72.7	468	6	ABP58275	Abp58275 Humanised
18	2232	72.7	451	8	ADH34584	Adh34584 008 heavy
19	2231.5	72.7	444	6	AAE35327	Aae35327 Humanised
20	2231.5	72.7	444	6	AAE34876	Aae34876 BIWA4/8 a
21	2231.5	72.7	444	8	ADL15443	Adl15443 Humanised
22	2231.5	72.7	444	8	ADO00851	Ado00851 Humanised
23	2229.5	72.6	475	7	ADM47075	Adm47075 Mouse ant
24	2229	72.6	451	8	ADP88494	Adp88494 Humanised
25	2226	72.5	449	3	AAY68810	Aay68810 A rat hea
26	2222.5	72.4	477	4	AAU14288	Aau14288 Human nov
27	2221.5	72.3	446	7	ADF11425	Adf11425 2D8 anti-
28	2220	72.3	474	5	AAO14065	Aao14065 Heavy cha
29	2220	72.3	474	6	ABU08017	Abu08017 Human mon
30	2220	72.3	474	7	ADF65775	Adf65775 Human mon
31	2220	72.3	474	8	ADJ92515	Adj92515 Human SOJ
32	2219.5	72.3	461	6	ABR39847	Abr39847 Hu266 N56
33	2219.5	72.3	461	6	ABR39843	Abr39843 Hu266 N56
34	2219	72.3	451	8	ADH34586	Adh34586 021 heavy
35	2216.5	72.2	442	6	ABR39465	Abr39465 Humanised
36	2216.5	72.2	442	6	ABU08311	Abu08311 Humanised
37	2216.5	72.2	442	6	ABB80109	Abb80109 Heavy cha
38	2216.5	72.2	442	7	ADE94066	Ade94066 Humanised
39	2216.5	72.2	442	8	ADN61714	Adn61714 Humanised
40	2216.5	72.2	461	4	AAU07745	Aau07745 Humanised
41	2216.5	72.2	461	6	ABR39844	Abr39844 Hu266 N56
42	2216.5	72.2	461	6	ABR39848	Abr39848 Hu266 N56
43	2216	72.2	451	4	AAE12715	Aae12715 Human rec
44	2216	72.2	451	6	ABU58807	Abu58807 Mucin 1 (
45	2212	72.0	445	7	ADF11421	Adf11421 2E11 anti

ALIGNMENTS

RESULT 1
AAB81987
ID AAB81987 standard; protein; 582 AA.
XX
AC AAB81987;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 53.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Claim 41; Page 168-172; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 582 AA;

Query Match 100.0%; Score 3071; DB 4; Length 582;
Best Local Similarity 100.0%; Pred. No. 2.1e-153;
Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60

Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYFDSWGQGTLLTVSSA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYFDSWGQGTLLTVSSA 120

Qy        121 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180

Qy        181 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 240

Qy        241 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300

Qy        301 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360

Qy        361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 420

Qy        421 QGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMILNGINNY 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 QGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMILNGINNY 480

Qy        481 KNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINV 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 KNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINV 540

Qy        541 IVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 582
              |||||||||||||||||||||||||||||||||||||||||||
Db        541 IVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 582
```

RESULT 2
AAB81991
ID AAB81991 standard; protein; 582 AA.
XX
AC AAB81991;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 57.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Claim 39; Page 175-179; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 582 AA;

```
  Query Match             98.5%;  Score 3026;  DB 4;  Length 582;
  Best Local Similarity   98.3%;  Pred. No. 4.9e-151;
  Matches  572;  Conservative    5;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60
              || |||||||||:|||||:||||||||||||||||||| | | ||||||||||||||||||
Db          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60

Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYFDSWGQGTLLTVSSA 120
              ||||||||||||||:|||||||||||||:||||:||||||||||||||||||| ||||||
Db         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSSA 120

Qy        121 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180

Qy        181 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 240

Qy        241 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300

Qy        301 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360

Qy        361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 420

Qy        421 QGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMILNGINNY 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 QGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMILNGINNY 480

Qy        481 KNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINV 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 KNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINV 540

Qy        541 IVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 582
              |||||||||||||||||||||||||||||||||||||||||||
Db        541 IVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 582
```

RESULT 3
AAB83156
ID AAB83156 standard; protein; 583 AA.
XX
AC AAB83156;
XX
DT 02-JUL-2001 (first entry)
XX
DE Ganglioside GM2 antibody-related protein #1.
XX
KW Ganglioside; GM2; antibody; cytostatic; cytotoxic; cancer.
XX
OS Unidentified.
XX

PN WO200123431-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006775.
XX
PR 30-SEP-1999; 99JP-00278292.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Nakamura K, Niwa R;
XX
DR WPI; 2001-266142/27.
XX
PT Monoclonal antibodies against ganglioside GM2 combined with drugs,
PT radioisotopes or proteins for treatment and diagnosis of cancer.
XX
PS Claim 43; Page 61-65; 80pp; Japanese.
XX
CC The present invention relates to derivatives of an antibody against
CC ganglioside GM2. The antibody may be a monoclonal antibody or its
CC fragments. The antibody is combined with a radioactive isotope, protein
CC or small drug in the treatment and diagnosis of cancer
XX
SQ Sequence 583 AA;

Query Match 90.5%; Score 2780.5; DB 4; Length 583;
Best Local Similarity 89.9%; Pred. No. 3.9e-138;
Matches 526; Conservative 22; Mismatches 32; Indels 5; Gaps 2;

Qy 1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60
Db 1 EVQLVQSGAEVKKPGASVKVSCKASGYTFTDYNMDWVKQSPGQGLEWMGYIYPNNGGTGY 60

Qy 61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTYY---FDSWGQGTLLTV 117
Db 61 NQKFKSKVTITVDTSTSTAYMELHSLRSEDTAVYYC--ATYGHYYGYMFAYWGQGTLVTV 118

Qy 118 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 177
Db 119 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 178

Qy 178 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 237
Db 179 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 238

Qy 238 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297
Db 239 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 298

Qy 298 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 357
Db 299 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 358

Qy 358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 417
Db 359 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 418

Qy 418 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMILNGI 477
Db 419 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMILNGI 478

Qy 478 NNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISN 537
Db 479 NNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISN 538

Qy 538 INVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 582
Db 539 INVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 583

RESULT 4
AAB81972

ID AAB81972 standard; protein; 581 AA.
XX
AC AAB81972;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD2 specific antibody related protein SEQ ID NO: 31.
XX
KW Ganglioside; GD2; complementation determining region; CDR; antibody;
KW mouse; cancer.
XX
OS Synthetic.
XX
PN WO200123573-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006773.
XX
PR 30-SEP-1999; 99JP-00278290.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266163/27.
XX
PT Human type complementation-determining domain transplanted antibody and
PT derivatives against ganglioside GD2, useful in diagnosis and therapy of
PT e.g. tumors, has low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Example 3; Page 111-114; 123pp; Japanese.
XX
CC The present invention describes an antibody, which can react specifically
CC with ganglioside GD2, and is transplanted with a human type
CC complementation-determining domain (CDR), or its fragments. The antibody
CC and its derivatives are useful in diagnosis and therapy of tumours,
CC particularly cancer diagnosis. The present sequence is a protein used in
CC the exemplification of the invention
XX
SQ Sequence 581 AA;

Query Match 89.9%; Score 2760.5; DB 4; Length 581;
Best Local Similarity 90.0%; Pred. No. 4.3e-137;
Matches 524; Conservative 22; Mismatches 35; Indels 1; Gaps 1;

Qy 1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60
Db 1 QVQLQESGPGLVKPSQTLSITCTVSGFSLASYNIHWVRQPPGKGLEWLGVIWAGGS-TNY 59

Qy 61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYFDSWGQGTLLTVSSA 120
Db 60 NSALMSRLTISKDNSKNQVFLKMSSLTAADTAVYYCAKRSDDYSWFAYWGQGTLVTVSSA 119

Qy 121 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180
Db 120 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 179

Qy 181 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 240
Db 180 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 239

Qy 241 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300
Db 240 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 299

Qy 301 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360
Db 300 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 359

Qy 361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 420

```
Db        360 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 419

Qy        421 QGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMILNGINNY 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 QGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMILNGINNY 479

Qy        481 KNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINV 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 KNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINV 539

Qy        541 IVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 582
              |||||||||||||||||||||||||||||||||||||||||||
Db        540 IVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 581


RESULT 5
AAE33444
ID   AAE33444 standard; protein; 579 AA.
XX
AC   AAE33444;
XX
DT   02-APR-2003  (first entry)
XX
DE   KS antibody heavy chain-interleukin 2 (IL-2) fusion protein.
XX
KW   Immunoglobulin; diagnosis; epithelial cell adhesion molecule; EpCAM;
KW   cancer; gene therapy; interleukin-2; IL2; fusion protein.
XX
OS   Unidentified.
XX
PN   WO200290566-A2.
XX
PD   14-NOV-2002.
XX
PF   03-MAY-2002; 2002WO-US013844.
XX
PR   03-MAY-2001; 2001US-0288564P.
XX
PA   (LEXI-) LEXIGEN PHARM CORP.
XX
PI   Gillies SD,  Lo K,  Qian X;
XX
DR   WPI; 2003-111985/10.
DR   N-PSDB; AAD51139.
XX
PT   New recombinant anti-EpCAM antibody having an amino acid sequence
PT   defining an immunoglobulin light or heavy chain framework region, useful
PT   for the diagnosis, prognosis and treatment of cancer.
XX
PS   Disclosure; Page 80-82; 82pp; English.
XX
CC   The present invention relates to novel recombinant anti-EpCAM (human
CC   epithelial cell adhesion molecule) antibodies comprising an amino acid
CC   sequence defining an immunoglobulin light or heavy chain framework
CC   region. Sequences of the present invention are useful for the diagnosis,
CC   prognosis and treatment of cancer. They are also used in gene therapy.
CC   The present sequence is KS antibody heavy chain-interleukin 2 (IL-2)
CC   fusion protein. This sequence is used to illustrate the method of the
CC   invention
XX
SQ   Sequence 579 AA;

  Query Match             89.6%;  Score 2750.5;  DB 6;  Length 579;
  Best Local Similarity   88.5%;  Pred. No. 1.4e-136;
  Matches  516;  Conservative   32;  Mismatches   30;  Indels    5;  Gaps    2;

Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60
              ::|||:|| :  :|| :::::|| |||: |::| |:||:| |||||:|: :|::      |
Db          1 QIQLVQSGAEVKKPGETVKISCKASGYTFTNYGMNWVKQTPGKGLKWMGWINTYTGEPTY 60

Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTR-VKLGTYYFDSWGQGTLLTVSS 119
                :|  ||||  | : | :| :||: :||:||:| ||| | :  | |    ||||| :||||
Db         61 ADDFKGRFAFSLETSTSTAFLQINNLRSEDTATYFCVRFISKGDY----WGQGTSVTVSS 116

Qy        120 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        117 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 176

Qy        180 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 239
              ||||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||
Db        177 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGG 236

Qy        240 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        237 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 296

Qy        300 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db        297 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE 356

Qy        360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 419
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        357 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 416

Qy        420 QQGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMILNGINN 479
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        417 QQGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMILNGINN 476

Qy        480 YKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNIN 539
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        477 YKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNIN 536

Qy        540 VIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 582
              |||||||||||||||||||||||||||||||||||||||||||
Db        537 VIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 579


RESULT 6
AAO30910
ID   AAO30910 standard; protein; 579 AA.
XX
AC   AAO30910;
XX
DT   22-SEP-2003  (first entry)
XX
DE   dI-KS-ala-IL2 (D20T) variant protein.
XX
KW   Cytokine; interleukin-2; IL-2; cancer; viral infection; immune disorder;
KW   gene therapy; immunoglobulin; Ig; fusion protein; human.
XX
OS   Homo sapiens.
OS   Unidentified.
OS   Chimeric.
XX
PN   WO2003048334-A2.
XX
PD   12-JUN-2003.
XX
PF   04-DEC-2002; 2002WO-US038780.
XX
PR   04-DEC-2001; 2001US-0337113P.
PR   12-APR-2002; 2002US-0371966P.
XX
PA   (EMDL-) EMD LEXIGEN RES CENT CORP.
XX
PI   Gillies SD;
XX
DR   WPI; 2003-513757/48.
XX
PT   New fusion protein comprising a non-IL-2 moiety fused to a mutant IL-2
PT   moiety, useful for preparing a composition for treating cancer, viral
PT   infections or immune disorders.
XX
PS   Example 10; Page 60-63; 71pp; English.
XX
CC   The invention relates to cytokine fusion proteins with increased
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CC   therapeutic index and methods for increasing the therapeutic index of
CC   such fusion proteins. The fusion protein comprises a non-interleukin-2
CC   (IL-2) moiety fused to a mutant IL-2 moiety. It is useful for preparing a
CC   composition for treating cancer, viral infections or immune disorders.
CC   The fusion protein is also used in gene therapy. The present sequence is
CC   dI-KS-ala-IL2 (D20T) variant protein comprising dI-KS heavy chain fused
CC   to human IL-2 (D20T) variant protein. This sequence is used to illustrate
CC   the method of the invention
XX
SQ   Sequence 579 AA;

  Query Match             89.6%;  Score 2750.5;  DB 6;  Length 579;
  Best Local Similarity   88.5%;  Pred. No. 1.4e-136;
  Matches  516;  Conservative   32;  Mismatches   30;  Indels    5;  Gaps    2;

Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60
              ::|||:|| :  :|| |:::|| |||: |::| |:|||||||||:|: :|::      |
Db          1 QIQLVQSGPELKKPGSSVKISCKASGYTFTNYGMNWVRQAPGKGLKWMGWINTYTGEPTY 60

Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTR-VKLGTYYFDSWGQGTLLTVSS 119
              :|  ||||||: : | :|||||: :||:||:| ||| | :  | |    ||||| :||||
Db         61 ADDFKGRFTITAETSTSTLYLQLNNLRSEDTATYFCVRFISKGDY----WGQGTTVTVSS 116

Qy        120 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        117 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 176

Qy        180 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 239
              |||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||
Db        177 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGG 236

Qy        240 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        237 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 296

Qy        300 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db        297 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE 356

Qy        360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 419
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        357 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 416

Qy        420 QQGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMILNGINN 479
              |||||||||||||||||||||| : :|| |||||||||||||||||| ||||||||||
Db        417 QQGNVFSCSVMHEALHNHYTQKSATATPGAAPTSSSTKKTQLQLEHLLLTLQMILNGINN 476

Qy        480 YKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNIN 539
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        477 YKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNIN 536

Qy        540 VIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 582
              |||||||||||||||||||||||||||||||||||||||||||
Db        537 VIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 579


RESULT 7
ADP42961
ID   ADP42961 standard; protein; 575 AA.
XX
AC   ADP42961;
XX
DT   23-SEP-2004  (first entry)
XX
DE   Humanised immunoglobulin heavy chain-IL-2 fusion protein SEQ ID NO:6.
XX
KW   immunoglobulin; variable region; antibody; GD2; cytostatic; gene therapy;
KW   cancer; cell surface glycosphingolipid; IL-2.
XX
OS   Synthetic.
XX
PN   WO2004055056-A1.
XX
PD   01-JUL-2004.
XX
PF   16-DEC-2003; 2003WO-EP014295.
XX
PR   17-DEC-2002; 2002US-0433945P.
XX
PA   (MERE ) MERCK PATENT GMBH.
XX
PI   Gillies SD,  Lo K;
XX
DR   WPI; 2004-488049/46.
DR   N-PSDB; ADP42959.
XX
PT   New modified m14.18 antibodies with reduced immunogenicity and that
PT   specifically bind the human cell surface glycosphingolipid GD2, useful
PT   for treating cancer.
XX
PS   Disclosure; SEQ ID NO 6; 51pp; English.
XX
CC   The invention relates to a novel antibody variable region, where the
CC   antibody variable region specifically binds to human cell surface
CC   glycosphingolipid GD2. An antibody variable region of the invention has
CC   cytostatic activity, and may have a use in gene therapy. The antibody may
CC   be used for treating cancer. The nucleic acid or cell is useful for
CC   manufacturing a medicament that may be used for treating diseases such as
CC   cancer. The present sequence represents an immunoglobulin heavy chain-IL-
CC   2 fusion protein.
XX
SQ   Sequence 575 AA;

  Query Match             88.6%;  Score 2719.5;  DB 8;  Length 575;
  Best Local Similarity   89.0%;  Pred. No. 6.1e-135;
  Matches  518;  Conservative   24;  Mismatches   33;  Indels    7;  Gaps    3;

Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60
              |||||:|| :  :|| |:::|| ||| :|: | |:|||  || |||:  |     || |
Db          1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY 60

Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYFDSWGQGTLLTVSSA 120
              :   ||| |:: | | :| |: ::|||:|.:|||:|     |  |   ||||| :|||||
Db         61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDTAVYYCVS---GMEY---WGQGTSVTVSSA 114

Qy        121 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 174

Qy        181 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 240
              |||||||||||||||||||||||||||||||||||:|||||||||||||||||||||||||
Db        175 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGP 234

Qy        241 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 294

Qy        301 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|:
Db        295 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM 354

Qy        361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 414

Qy        421 QGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMILNGINNY 480
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        415 QGNVFSCSVMHEALHNHYTQKSLSLSPG-APTSSSTKKTQLQLEHLLLDLQMILNGINNY 473

Qy        481 KNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINV 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 KNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINV 533

Qy        541 IVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 582
              |||||||||||||||||||||||||||||||||||||||||||
Db        534 IVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 575
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RESULT 8
AAO30915
ID   AAO30915 standard; protein; 580 AA.
XX
AC   AAO30915;
XX
DT   22-SEP-2003  (first entry)
XX
DE   dI-NHS76 (gamma4h) (FN>AQ)-ala-IL2 (D20T) variant protein.
XX
KW   Cytokine; interleukin-2; IL-2; cancer; viral infection; immune disorder;
KW   gene therapy; immunoglobulin; Ig; fusion protein; human; variant.
XX
OS   Homo sapiens.
OS   Unidentified.
OS   Chimeric.
XX
PN   WO2003048334-A2.
XX
PD   12-JUN-2003.
XX
PF   04-DEC-2002; 2002WO-US038780.
XX
PR   04-DEC-2001; 2001US-0337113P.
PR   12-APR-2002; 2002US-0371966P.
XX
PA   (EMDL-) EMD LEXIGEN RES CENT CORP.
XX
PI   Gillies SD;
XX
DR   WPI; 2003-513757/48.
XX
PT   New fusion protein comprising a non-IL-2 moiety fused to a mutant IL-2
PT   moiety, useful for preparing a composition for treating cancer, viral
PT   infections or immune disorders.
XX
PS   Example 10; Page 68-71; 71pp; English.
XX
CC   The invention relates to cytokine fusion proteins with increased
CC   therapeutic index and methods for increasing the therapeutic index of
CC   such fusion proteins. The fusion protein comprises a non-interleukin-2
CC   (IL-2) moiety fused to a mutant IL-2 moiety. It is useful for preparing a
CC   composition for treating cancer, viral infections or immune disorders.
CC   The fusion protein is also used in gene therapy. The present sequence is
CC   dI-NHS76 (gamma4h) (FN>AQ)-ala-IL2 (D20T) variant protein comprising dI-
CC   KS heavy chain fused to human IL-2 (D20T) variant protein. This sequence
CC   is used to illustrate the method of the invention
XX
SQ   Sequence 580 AA;

  Query Match             85.3%;  Score 2621;  DB 6;  Length 580;
  Best Local Similarity   85.8%;  Pred. No. 9.2e-130;
  Matches  500;  Conservative   29;  Mismatches   50;  Indels    4;  Gaps    3;

Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSH-YAMSWVRQAPGKGLEWVAYISSGGSGTY 59
              :||| |||   |:|  :| ::|| ||:: |  |   |:|| |||||||:  |   || ||
Db          1 QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYWGWIRQPPGKGLEWIGSIYHSGS-TY 59

Qy         60 YSDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYFDSWGQGTLLTVSS 119
              |: |:| | ||| | |||   |:: |: | |:|||:| | |     || |||||:||||
Db         60 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGKWSK--FDYWGQGTLVTVSS 117

Qy        120 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
              |||||||||||||| |:|||  ||||||||||||||||||||||||||||||||||||||
Db        118 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 177

Qy        180 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 239
              |||||||||||||||||:|| |||:||||||||||:|||||||||||||||||||| |||
Db        178 GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEFLGG 237

Qy        240 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299
              |||||||||||||||||||||||||||||||||||||||| |||||:|||||||||||||||
Db        238 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQAQ 297

Qy        300 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359
              |||||||||||||||||||||||||||||||| ||: |||||||||||||||||||::|
Db        298 STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEE 357

Qy        360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 419
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 417

Qy        420 QQGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMILNGINN 479
              ||||:|||||||||||||||| : :|| |||||||||||||||| ||||||||||
Db        418 QQGNIFSCSVMHEALHNHYTQKSATATPGAAPTSSSTKKTQLQLEHLLLTLQMILNGINN 477

Qy        480 YKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNIN 539
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 YKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNIN 537

Qy        540 VIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 582
              |||||||||||||||||||||||||||||||||||||||||||
Db        538 VIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 580


RESULT 9
AAO30913
ID   AAO30913 standard; protein; 580 AA.
XX
AC   AAO30913;
XX
DT   22-SEP-2003  (first entry)
XX
DE   dI-NHS76 (gamma2h) (FN>AQ)-ala-IL2 (D20T) variant protein.
XX
KW   Cytokine; interleukin-2; IL-2; cancer; viral infection; immune disorder;
KW   gene therapy; immunoglobulin; Ig; fusion protein; human; variant.
XX
OS   Homo sapiens.
OS   Unidentified.
OS   Chimeric.
XX
PN   WO2003048334-A2.
XX
PD   12-JUN-2003.
XX
PF   04-DEC-2002; 2002WO-US038780.
XX
PR   04-DEC-2001; 2001US-0337113P.
PR   12-APR-2002; 2002US-0371966P.
XX
PA   (EMDL-) EMD LEXIGEN RES CENT CORP.
XX
PI   Gillies SD;
XX
DR   WPI; 2003-513757/48.
XX
PT   New fusion protein comprising a non-IL-2 moiety fused to a mutant IL-2
PT   moiety, useful for preparing a composition for treating cancer, viral
PT   infections or immune disorders.
XX
PS   Claim 37; Page 64-67; 71pp; English.
XX
CC   The invention relates to cytokine fusion proteins with increased
CC   therapeutic index and methods for increasing the therapeutic index of
CC   such fusion proteins. The fusion protein comprises a non-interleukin-2
CC   (IL-2) moiety fused to a mutant IL-2 moiety. It is useful for preparing a
CC   composition for treating cancer, viral infections or immune disorders.
CC   The fusion protein is also used in gene therapy. The present sequence is
CC   dI-NHS76 (gamma2h) (FN>AQ)-ala-IL2 (D20T) variant protein comprising dI-
CC   KS heavy chain fused to human IL-2 (D20T) variant protein. This sequence
CC   is used to illustrate the method of the invention
XX
SQ   Sequence 580 AA;
```

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  Query Match             84.3%;  Score 2589;  DB 6;  Length 580;
  Best Local Similarity   85.1%;  Pred. No. 4.4e-128;
  Matches  497;  Conservative   29;  Mismatches   52;  Indels    6;  Gaps    5;

Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSH-YAMSWVRQAPGKGLEWVAYISSGGSGTY 59
              :||| |||   |:|  :| ::|| ||:: |  |   |:|| |||||||:  |   || ||
Db          1 QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYWGWIRQPPGKGLEWIGSIYHSGS-TY 59

Qy         60 YSDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYFDSWGQGTLLTVSS 119
              |: |:| | ||| | |||   |:: |: | |:|||:| | |     || ||||||:||||
Db         60 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGKWSK--FDYWGQGTLVTVSS 117

Qy        120 -ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 178
               |||||||||||||| |:||| ||||||||||||||||||||||||||||||||||||||
Db        118 GASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 177

Qy        179 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 238
              |||||||||||||||: ||||| |||:|||||||||| ||||||||||||||||||  :
Db        178 SGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVEPKSCDKTHTCPPCPAPP-VA 236

Qy        239 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 298
              ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db        237 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQA 296

Qy        299 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 358
              ||:||||||||:|||||||||||||||| |||||||||| |||||||||||||||||:
Db        297 QSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSRE 356

Qy        359 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 418
              |:||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db        357 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSR 416

Qy        419 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMILNGIN 478
              |||||||||||||||||||||| : :|| |||||||||||||||||| |||||||||
Db        417 WQQGNVFSCSVMHEALHNHYTQKSATATPGAAPTSSSTKKTQLQLEHLLLTLQMILNGIN 476

Qy        479 NYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNI 538
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        477 NYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNI 536

Qy        539 NVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 582
              |||||||||||||||||||||||||||||||||||||||||||||
Db        537 NVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 580


RESULT 10
AAE33522
ID   AAE33522 standard; protein; 447 AA.
XX
AC   AAE33522;
XX
DT   02-APR-2003  (first entry)
XX
DE   Human AQC2 heavy chain protein.
XX
KW   Human; very late activation antigen; VLA-1; beta1 containing integrin;
KW   immunological disorder; inflammatory disorder; skin related condition;
KW   psoriasis; eczema; burn; dermatitis; respiratory distress syndrome;
KW   fibrosis; allergic rhinitis; asthma; bronchitis; tendonitis; bursitis;
KW   fever; migraine headache; inflammatory bowel disease; Crohn's disease;
KW   irritable bowel syndrome; colitis; colorectal cancer; vascular disease;
KW   atherosclerosis; thyroiditis; aplastic anaemia; periarteritis nodosa;
KW   gastritis; Hodgkin's disease; rheumatic fever; autoimmune disease;
KW   osteoarthritis; type I diabetes; myasthenia gravis; rheumatoid arthritis;
KW   systemic lupus erythematosus; multiple sclerosis; nephrotic syndrome;
KW   renal failure; sarcoidosis; Behcet's syndrome; gingivitis; polymyositis;
KW   hypersensitivity; graft rejection; transplant rejection; conjunctivitis;
KW   graft versus host disease; myocardial ischaemia.
XX
OS   Homo sapiens.
XX
PN   WO200283854-A2.
XX
PD   24-OCT-2002.
XX
PF   12-APR-2002; 2002WO-US011521.
XX
PR   13-APR-2001; 2001US-0283794P.
PR   06-JUL-2001; 2001US-0303689P.
XX
PA   (BIOJ ) BIOGEN INC.
XX
PI   Lyne PD,  Garber EA,  Saldanha JW,  Karpusas M;
XX
DR   WPI; 2003-093009/08.
XX
PT   New anti-VLA-1 antibodies are useful for preventing or treating VLA-1-
PT   mediated immunological or inflammatory disorders, e.g. psoriasis, eczema,
PT   burns, dermatitis, and abnormal proliferation of hair follicle cells or
PT   fibrosis.
XX
PS   Claim 6; Page 75; 248pp; English.
XX
CC   The present invention relates to novel antibodies that specifically bind
CC   to very late activation (VLA-1; beta1 containing integrins) antigens and
CC   methods of using these antibodies to treat immunological disorders. The
CC   anti-VLA-1 antibodies are useful for preventing or treating VLA-1-
CC   mediated immunological or inflammatory disorders such as skin related
CC   conditions (e.g. psoriasis, eczema, burns, dermatitis and abnormal
CC   proliferation of hair follicle cells), fibrosis (e.g. kidney or lung
CC   fibrosis), allergic rhinitis, respiratory distress syndrome, asthma,
CC   bronchitis, tendonitis, bursitis, fever, migraine headaches, gastro-
CC   intestinal conditions (e.g. inflammatory bowel disease, Crohn's disease,
CC   gastritis, irritable bowel syndrome, colitis and colorectal cancer),
CC   vascular diseases (e.g. atherosclerosis), thyroiditis, aplastic anaemia,
CC   periarteritis nodosa, Hodgkin's disease, rheumatic fever, osteoarthritis,
CC   autoimmune diseases (e.g. type I diabetes, myasthenia gravis, rheumatoid
CC   arthritis, systemic lupus erythematosus and multiple sclerosis), renal
CC   failure, sarcoidosis, nephrotic syndrome, Behcet's syndrome, gingivitis,
CC   polymyositis, hypersensitivity (e.g. delayed type hypersensitivity or
CC   immediate hypersensitivity), graft and transplant rejections, graft
CC   versus host disease, conjunctivitis, swelling occurring after injury,
CC   myocardial ischaemia or endotoxin shock syndrome. The present sequence is
CC   human AQC2 heavy chain protein
XX
SQ   Sequence 447 AA;

  Query Match             73.2%;  Score 2246.5;  DB 6;  Length 447;
  Best Local Similarity   95.1%;  Pred. No. 3.3e-110;
  Matches  426;  Conservative    4;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60
              |||||||||  ||||||||:||||||| || | |||||||||||||||| || ||  |||
Db          1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSRYTMSWVRQAPGKGLEWVATISGGGH-TYY 59

Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYFDSWGQGTLLTVSSA 120
              |||||||||||||||||||| ||||||:|||:|||       ||| ||||||:|||||
Db         60 LDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRGFGDGGYFDVWGQGTLVTVSSA 119

Qy        121 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 179

Qy        181 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 239

Qy        241 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 299

Qy        301 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 359
```

```
Qy        361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 419

Qy        421 QGNVFSCSVMHEALHNHYTQKSLSLSPG 448
              ||||||||||||||||||||||||||||
Db        420 QGNVFSCSVMHEALHNHYTQKSLSLSPG 447
```

RESULT 11
AAE33523
ID AAE33523 standard; protein; 447 AA.
XX
AC AAE33523;
XX
DT 02-APR-2003 (first entry)
XX
DE Human AQC2 heavy chain mutant protein, haAQC2.
XX
KW Human; very late activation antigen; VLA-1; beta1 containing integrin; immunological disorder; inflammatory disorder; skin related condition; psoriasis; eczema; burn; dermatitis; respiratory distress syndrome; fibrosis; allergic rhinitis; asthma; bronchitis; tendonitis; bursitis; fever; migraine headache; inflammatory bowel disease; Crohn's disease; irritable bowel syndrome; colitis; colorectal cancer; vascular disease; atherosclerosis; thyroiditis; aplastic anaemia; periarteritis nodosa; gastritis; Hodgkin's disease; rheumatic fever; autoimmune disease; osteoarthritis; type I diabetes; myasthenia gravis; rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis; nephrotic syndrome; renal failure; sarcoidosis; Behcet's syndrome; gingivitis; polymyositis; hypersensitivity; graft rejection; transplant rejection; conjunctivitis; graft versus host disease; myocardial ischaemia; mutant; mutein.
XX
OS Homo sapiens.
XX
PN WO200283854-A2.
XX
PD 24-OCT-2002.
XX
PF 12-APR-2002; 2002WO-US011521.
XX
PR 13-APR-2001; 2001US-0283794P.
PR 06-JUL-2001; 2001US-0303689P.
XX
PA (BIOJ) BIOGEN INC.
XX
PI Lyne PD, Garber EA, Saldanha JW, Karpusas M;
XX
DR WPI; 2003-093009/08.
XX
PT New anti-VLA-1 antibodies are useful for preventing or treating VLA-1-
PT mediated immunological or inflammatory disorders, e.g. psoriasis, eczema,
PT burns, dermatitis, and abnormal proliferation of hair follicle cells or
PT fibrosis.
XX
PS Example 23; Page 91-92; 248pp; English.
XX
CC The present invention relates to novel antibodies that specifically bind
CC to very late activation (VLA-1; beta1 containing integrins) antigens and
CC methods of using these antibodies to treat immunological disorders. The
CC anti-VLA-1 antibodies are useful for preventing or treating VLA-1-
CC mediated immunological or inflammatory disorders such as skin related
CC conditions (e.g. psoriasis, eczema, burns, dermatitis and abnormal
CC proliferation of hair follicle cells), fibrosis (e.g. kidney or lung
CC fibrosis), allergic rhinitis, respiratory distress syndrome, asthma,
CC bronchitis, tendonitis, bursitis, fever, migraine headaches, gastro-
CC intestinal conditions (e.g. inflammatory bowel disease, Crohn's disease,
CC gastritis, irritable bowel syndrome, colitis and colorectal cancer),
CC vascular diseases (e.g. atherosclerosis), thyroiditis, aplastic anaemia,
CC periarteritis nodosa, Hodgkin's disease, rheumatic fever, osteoarthritis,
CC autoimmune diseases (e.g. type I diabetes, myasthenia gravis, rheumatoid
CC arthritis, systemic lupus erythematosus and multiple sclerosis), renal
CC failure, sarcoidosis, nephrotic syndrome, Behcet's syndrome, gingivitis,
CC polymyositis, hypersensitivity (e.g. delayed type hypersensitivity or
CC immediate hypersensitivity), graft and transplant rejections, graft
CC versus host disease, conjunctivitis, swelling occurring after injury,
CC myocardial ischaemia or endotoxin shock syndrome. The present sequence is
CC human AQC2 heavy chain mutant protein, haAQC2
XX
SQ Sequence 447 AA;

```
  Query Match             73.0%;  Score 2240.5;  DB 6;  Length 447;
  Best Local Similarity   94.9%;  Pred. No. 6.8e-110;
  Matches  425;  Conservative    4;  Mismatches   18;  Indels    1;  Gaps    1;

Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60
              |||||||||  ||||||||:|||||||  ||  |  ||||||||||||||||  ||  ||  |||
Db          1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSRYTMSWVRQAPGKGLEWVATISGGGH-TYY 59

Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYFDSWGQGTLLTVSSA 120
              |||||||||||||||||||||| ||||||:|||:|||       ||| ||||||:|||||
Db         60 LDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRGFGDGGYFDVWGQGTLVTVSSA 119

Qy        121 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 179

Qy        181 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 239

Qy        241 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        240 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYQS 299

Qy        301 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 359

Qy        361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 419

Qy        421 QGNVFSCSVMHEALHNHYTQKSLSLSPG 448
              ||||||||||||||||||||||||||||
Db        420 QGNVFSCSVMHEALHNHYTQKSLSLSPG 447
```

RESULT 12
AAO18400
ID AAO18400 standard; protein; 449 AA.
XX
AC AAO18400;
XX
DT 11-OCT-2002 (first entry)
XX
DE Mature humanised murine CBE11 heavy chain variable domain.
XX
KW Mouse; humanised antibody; lymphotoxin beta receptor; antibody; cancer; neoplasia; LT-beta-R; light chain; heavy chain; variable region.
XX
OS Mus sp.
OS Synthetic.
XX
PN WO200230986-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-US032140.
XX
PR 13-OCT-2000; 2000US-0240285P.
PR 13-MAR-2001; 2001US-0275289P.
PR 21-JUN-2001; 2001US-0299987P.
XX
PA (BIOJ) BIOGEN INC.
XX

```
PI   Garber E,  Lyne P,  Saldanha JW;
XX
DR   WPI; 2002-583337/62.
XX
PT   New humanized anti-lymphotoxin-beta receptor antibody, useful for
PT   treating or reducing the advancement, severity or effects of neoplasia,
PT   particularly solid tumors (i.e. carcinomas) including colorectal cancer
PT   and breast cancer.
XX
PS   Example 5; Page 25-26; 41pp; English.
XX
CC   The present invention relates to humanised anti-lymphotoxin beta receptor
CC   (LT-beta-R) antibodies. These are derived from the murine LT-beta-R
CC   binding antibody CBE11 and can be used to treat neoplasia in humans. The
CC   present sequence is a humanised murine CBE11 heavy chain variable region
XX
SQ   Sequence 449 AA;

  Query Match             72.9%;  Score 2238.5;  DB 5;  Length 449;
  Best Local Similarity   94.0%;  Pred. No. 8.7e-110;
  Matches  422;  Conservative    8;  Mismatches   18;  Indels    1;  Gaps    1;

Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60
              |||||||||  |:||||||:||||||| || | | | ||||||||||||| || ||| |||
Db          1 EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMYWFRQAPGKGLEWVATISDGGSYTYY 60

Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGT-YYFDSWGQGTLLTVSS 119
                |||||||||||||:||:||||| ||||||:|||:| | : |  |||| ||||| :||||
Db         61 PDSVKGRFTISRDNAKNSLYLQMSSLRAEDTAVYYCAREENGNFYYFDYWGQGTTVTVSS 120

Qy        120 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 180

Qy        180 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 240

Qy        240 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 300

Qy        300 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 360

Qy        360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 419
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 420

Qy        420 QQGNVFSCSVMHEALHNHYTQKSLSLSPG 448
              |||||||||||||||||||||||||||||
Db        421 QQGNVFSCSVMHEALHNHYTQKSLSLSPG 449


RESULT 13
AAE33524
ID   AAE33524 standard; protein; 447 AA.
XX
AC   AAE33524;
XX
DT   02-APR-2003  (first entry)
XX
DE   Human AQC2 heavy chain mutant protein, hsAQC2.
XX
KW   Human; very late activation antigen; VLA-1; beta1 containing integrin;
KW   immunological disorder; inflammatory disorder; skin related condition;
KW   psoriasis; eczema; burn; dermatitis; respiratory distress syndrome;
KW   fibrosis; allergic rhinitis; asthma; bronchitis; tendonitis; bursitis;
KW   fever; migraine headache; inflammatory bowel disease; Crohn's disease;
KW   irritable bowel syndrome; colitis; colorectal cancer; vascular disease;
KW   atherosclerosis; thyroiditis; aplastic anaemia; periarteritis nodosa;
KW   gastritis; Hodgkin's disease; rheumatic fever; autoimmune disease;
KW   osteoarthritis; type I diabetes; myasthenia gravis; rheumatoid arthritis;
KW   systemic lupus erythematosus; multiple sclerosis; nephrotic syndrome;
KW   renal failure; sarcoidosis; Behcet's syndrome; gingivitis; polymyositis;
KW   hypersensitivity; graft rejection; transplant rejection; conjunctivitis;
KW   graft versus host disease; myocardial ischaemia; mutant; mutein.
XX
OS   Homo sapiens.
XX
PN   WO200283854-A2.
XX
PD   24-OCT-2002.
XX
PF   12-APR-2002; 2002WO-US011521.
XX
PR   13-APR-2001; 2001US-0283794P.
PR   06-JUL-2001; 2001US-0303689P.
XX
PA   (BIOJ ) BIOGEN INC.
XX
PI   Lyne PD,  Garber EA,  Saldanha JW,  Karpusas M;
XX
DR   WPI; 2003-093009/08.
XX
PT   New anti-VLA-1 antibodies are useful for preventing or treating VLA-1-
PT   mediated immunological or inflammatory disorders, e.g. psoriasis, eczema,
PT   burns, dermatitis, and abnormal proliferation of hair follicle cells or
PT   fibrosis.
XX
PS   Example 23; Page 92; 248pp; English.
XX
CC   The present invention relates to novel antibodies that specifically bind
CC   to very late activation (VLA-1; beta1 containing integrins) antigens and
CC   methods of using these antibodies to treat immunological disorders. The
CC   anti-VLA-1 antibodies are useful for preventing or treating VLA-1-
CC   mediated immunological or inflammatory disorders such as skin related
CC   conditions (e.g. psoriasis, eczema, burns, dermatitis and abnormal
CC   proliferation of hair follicle cells), fibrosis (e.g. kidney or lung
CC   fibrosis), allergic rhinitis, respiratory distress syndrome, asthma,
CC   bronchitis, tendonitis, bursitis, fever, migraine headaches, gastro-
CC   intestinal conditions (e.g. inflammatory bowel disease, Crohn's disease,
CC   gastritis, irritable bowel syndrome, colitis and colorectal cancer),
CC   vascular diseases (e.g. atherosclerosis), thyroiditis, aplastic anaemia,
CC   periarteritis nodosa, Hodgkin's disease, rheumatic fever, osteoarthritis,
CC   autoimmune diseases (e.g. type I diabetes, myasthenia gravis, rheumatoid
CC   arthritis, systemic lupus erythematosus and multiple sclerosis), renal
CC   failure, sarcoidosis, nephrotic syndrome, Behcet's syndrome, gingivitis,
CC   polymyositis, hypersensitivity (e.g. delayed type hypersensitivity or
CC   immediate hypersensitivity), graft and transplant rejections, graft
CC   versus host disease, conjunctivitis, swelling occurring after injury,
CC   myocardial ischaemia or endotoxin shock syndrome. The present sequence is
CC   human AQC2 heavy chain mutant protein, hsAQC2
XX
SQ   Sequence 447 AA;

  Query Match             72.8%;  Score 2236.5;  DB 6;  Length 447;
  Best Local Similarity   94.6%;  Pred. No. 1.1e-109;
  Matches  424;  Conservative    4;  Mismatches   19;  Indels    1;  Gaps    1;

Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60
              |||||||||  ||||||||:||||||| || | |||||||||||||||| || ||  |||
Db          1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSRYTMSWVRQAPGKGLEWVATISGGGH-TYY 59

Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYFDSWGQGTLLTVSSA 120
              |||||||||||||||||||||| ||||||:|||:|||       ||| ||||||:|||||
Db         60 LDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRGFGDGGYFDVWGQGTLVTVSSA 119

Qy        121 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 179

Qy        181 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        180 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGP 239
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```
Qy        241 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 299

Qy        301 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 359

Qy        361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 419

Qy        421 QGNVFSCSVMHEALHNHYTQKSLSLSPG 448
              ||||||||||||||||||||||||||||
Db        420 QGNVFSCSVMHEALHNHYTQKSLSLSPG 447
```

RESULT 14
ADH34587
ID ADH34587 standard; protein; 450 AA.
XX
AC ADH34587;
XX
DT 11-MAR-2004 (first entry)
XX
DE 023 heavy chain.
XX
KW antibody; OX40 receptor; specific phage antibody; scFv; CD134; ACT-4;
KW ACT35; TNF receptor family; CD4+; T cell; tumour necrosis factor;
KW proliferation; immune response; memory cell; tumour; bacterial; viral;
KW antigen; leukaemia; neoplasm; bile duct carcinoma; bladder carcinoma;
KW severe acute respiratory syndrome; SARS; herpes simplex virus; HSV;
KW hepatitis B virus; HBV; HIV; Mycobacterium tuberculosis;
KW Pseudomonas aeruginosa; Vibrio cholerae.
XX
OS Synthetic.
XX
PN WO2003106498-A2.
XX
PD 24-DEC-2003.
XX
PF 13-JUN-2003; 2003WO-EP006341.
XX
PR 13-JUN-2002; 2002WO-NL000389.
XX
PA (CRUC-) CRUCELL HOLLAND BV.
XX
PI Bakker ABH, Meester-Rood PML, Bakker AQ;
XX
DR WPI; 2004-082162/08.
DR N-PSDB; ADH34601.
XX
PT Novel agonistic binding molecule capable of binding to and stimulating
PT human OX-40-receptor, useful for modulating T-cell proliferation.
XX
PS Claim 4; SEQ ID NO 28; 148pp; English.
XX
CC This sequence represents the heavy chain of a selected phage antibody
CC against human OX40 receptor. OX40 receptor, (also known as CD134, ACT-4,
CC ACT35) is a member of the TNF receptor family which is expressed on
CC activated CD4+ T cells. Triggering of this receptor enhances the
CC proliferation of CD4+ T-cells during an immune response and influences
CC the formation of CD4+ memory cells. A human OX40 receptor specific phage
CC antibody (scFv) represents the agonistic binding molecule of the
CC invention which is capable of binding to and stimulating the human OX-40-
CC receptor. The binding molecules of the invention are useful as a
CC medicament for treating neoplastic, viral or bacterial disorder or
CC disease, for stimulating T-cells in vitro and for enhancing the immune
CC response in a human or animal against a tumour, bacterial or viral
CC antigen. They are useful for modulating T-cell response in a human which
CC involves, administration to the human, where the modulation includes
CC stimulation of T-cells. A pharmaceutical composition containing the
CC binding molecules is useful for preventing and treating neoplastic
CC disorder or disease such as leukaemias, neoplasm, bile duct carcinoma,
CC bladder carcinoma, viral disorder or disease associated with severe acute
CC respiratory syndrome (SARS), herpes simplex virus (HSV), hepatitis B
CC virus (HBV), HIV and bacterial disorder or disease associated with
CC Mycobacterium tuberculosis, Pseudomonas aeruginosa and Vibrio cholerae.
XX
SQ Sequence 450 AA;

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  Query Match             72.8%;  Score 2236.5;  DB 8;  Length 450;
  Best Local Similarity   93.1%;  Pred. No. 1.1e-109;
  Matches  420;  Conservative   12;  Mismatches   16;  Indels    3;  Gaps    2;

Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60
              |||||||||  | ||||||:||| ||| || ||| |||||||||||||: | :|| ||||
Db          1 EVQLVESGGGLVHPGGSLRLSCAGSGFTFSSYAMHWVRQAPGKGLEWVSAIGTGG-GTYY 59

Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVK--LGTYYFDSWGQGTLLTVS 118
              :||| |||||||||||||||| ||||||:|||:| |    :| |:|| |||||||:|||
Db         60 ADSVMGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARYDNVMGLYWFDYWGQGTLVTVS 119

Qy        119 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 179

Qy        179 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 238
              ||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||||
Db        180 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLG 239

Qy        239 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 299

Qy        299 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 358
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Db        300 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE 359

Qy        359 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 418
              |:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 419

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Db        420 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 450
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RESULT 15
AAO31101
ID AAO31101 standard; protein; 445 AA.
XX
AC AAO31101;
XX
DT 06-OCT-2003 (first entry)
XX
DE Human A2-G8 SCF antibody heavy chain variable and constant region.
XX
KW Human; antibody; stem cell factor; mast cell growth factor; asthma; SCF;
KW steel factor; c-kit ligand; gene therapy.
XX
OS Homo sapiens.
XX
PN WO2003051311-A2.
XX
PD 26-JUN-2003.
XX
PF 16-DEC-2002; 2002WO-US040227.
XX
PR 17-DEC-2001; 2001US-0342174P.
XX
PA (FARB) BAYER CORP.
XX
PI Takeuchi T, Tomkinson A, Neben S;
XX

DR WPI; 2003-523500/49.
XX
PT New purified human antibody that binds to stem cell factor protein,
PT useful for preparing a composition for treating asthma.
XX
PS Claim 9; Page 47; 94pp; English.
XX
CC The invention provides human antibodies that bind to stem cell factor
CC (SCF) protein. SCF is also known as mast cell growth factor, steel factor
CC or c-kit ligand. Antibodies of the invention are useful for preparing
CC compositions for treating asthma. They are also used in gene therapy. The
CC present sequence is human SCF antibody heavy chain variable and constant
CC region
XX
SQ Sequence 445 AA;

Query Match 72.8%; Score 2234.5; DB 6; Length 445;
Best Local Similarity 94.4%; Pred. No. 1.4e-109;
Matches 421; Conservative 7; Mismatches 17; Indels 1; Gaps 1;

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Db          1 LVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADS 60

Qy         64 VKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYFDSWGQGTLLTVSSASTK 123
              |||||||||||||||||| ||||||:|||:| |      :|| |||||||:||||||||
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Qy        124 GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS 183
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Db        120 GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS 179

Qy        184 LSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVF 243
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Qy        244 LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR 303
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Qy        304 VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKN 363
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Qy        364 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN 423
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Db        360 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN 419

Qy        424 VFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||||||||||
Db        420 VFSCSVMHEALHNHYTQKSLSLSPGK 445
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Search completed: December 23, 2004, 18:57:36
Job time : 160.692 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2004, 18:46:39 ; Search time 38.4376 Seconds
(without alignments)
1004.148 Million cell updates/sec

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Perfect score: 3071
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2194.5	71.5	452	3	US-09-027-449-71	Sequence 71, Appl
2	2194.5	71.5	452	3	US-09-026-985-71	Sequence 71, Appl
3	2194.5	71.5	452	4	US-09-121-952A-71	Sequence 71, Appl
4	2194.5	71.5	452	4	US-09-234-340A-71	Sequence 71, Appl
5	2194.5	71.5	459	1	US-08-157-101A-7	Sequence 7, Appli
6	2169	70.6	453	3	US-08-466-151-8	Sequence 8, Appli
7	2169	70.6	453	3	US-08-466-163B-8	Sequence 8, Appli
8	2169	70.6	453	4	US-09-802-096-8	Sequence 8, Appli
9	2169	70.6	453	4	US-09-802-077-8	Sequence 8, Appli
10	2167	70.6	451	2	US-08-887-352B-14	Sequence 14, Appl
11	2167	70.6	451	2	US-08-887-352B-16	Sequence 16, Appl
12	2167	70.6	451	3	US-08-466-151-65	Sequence 65, Appl
13	2167	70.6	451	3	US-09-109-207C-14	Sequence 14, Appl
14	2167	70.6	451	3	US-09-109-207C-16	Sequence 16, Appl
15	2167	70.6	451	3	US-09-296-005-14	Sequence 14, Appl
16	2167	70.6	451	3	US-09-296-005-16	Sequence 16, Appl
17	2167	70.6	451	4	US-09-920-171-14	Sequence 14, Appl
18	2167	70.6	451	4	US-09-920-171-16	Sequence 16, Appl
19	2167	70.6	451	4	US-09-716-028-14	Sequence 14, Appl
20	2167	70.6	451	4	US-09-716-028-16	Sequence 16, Appl
21	2167	70.6	451	4	US-10-113-996-14	Sequence 14, Appl
22	2167	70.6	451	4	US-10-113-996-16	Sequence 16, Appl
23	2163	70.4	451	2	US-08-887-352B-18	Sequence 18, Appl
24	2163	70.4	451	3	US-09-109-207C-18	Sequence 18, Appl
25	2163	70.4	451	3	US-09-282-505-2	Sequence 2, Appli
26	2163	70.4	451	3	US-09-054-255-2	Sequence 2, Appli
27	2163	70.4	451	3	US-09-296-005-18	Sequence 18, Appl
28	2163	70.4	451	4	US-09-282-846-2	Sequence 2, Appli
29	2163	70.4	451	4	US-09-680-145-2	Sequence 2, Appli
30	2163	70.4	451	4	US-09-920-171-18	Sequence 18, Appl
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32	2163	70.4	451	4	US-09-483-588-2	Sequence 2, Appli
33	2163	70.4	451	4	US-10-113-996-18	Sequence 18, Appl
34	2160.5	70.4	449	3	US-09-679-397-2	Sequence 2, Appli
35	2160.5	70.4	449	4	US-09-680-148-2	Sequence 2, Appli
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37	2140	69.7	478	3	US-08-487-550-8	Sequence 8, Appli
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40	2127	69.3	449	1	US-08-458-516-13	Sequence 13, Appl
41	2084.5	67.9	467	4	US-08-030-175-42	Sequence 42, Appl
42	2084	67.9	711	3	US-09-485-737B-90	Sequence 90, Appl
43	2081.5	67.8	467	4	US-08-030-175-41	Sequence 41, Appl
44	2081	67.8	468	3	US-09-485-737B-67	Sequence 67, Appl
45	2080	67.7	476	2	US-08-378-939-10	Sequence 10, Appl

ALIGNMENTS

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RESULT 1
US-09-027-449-71
; Sequence 71, Application US/09027449
; Patent No. 6025158
;  GENERAL INFORMATION:
;    APPLICANT:  Gonzalez, Tania R.
;    APPLICANT:  Leong, Steven R.
;    APPLICANT:  Presta, Leonard G.
;    TITLE OF INVENTION:  Antibody Fragment-Polymer Conjugates and
;    TITLE OF INVENTION:  Humanized Anti-IL-8 Monoclonal Antibodies
;    NUMBER OF SEQUENCES:  72
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/027,449
;      FILING DATE:  20-Feb-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/074,330
;      FILING DATE:  22-Jan-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/038,664
;      FILING DATE:  21-Feb-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  P1085R3-2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-5530
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  71:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  452 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-09-027-449-71

  Query Match             71.5%;  Score 2194.5;  DB 3;  Length 452;
  Best Local Similarity   90.9%;  Pred. No. 2.3e-161;
  Matches  411;  Conservative   14;  Mismatches   24;  Indels    3;  Gaps    1;
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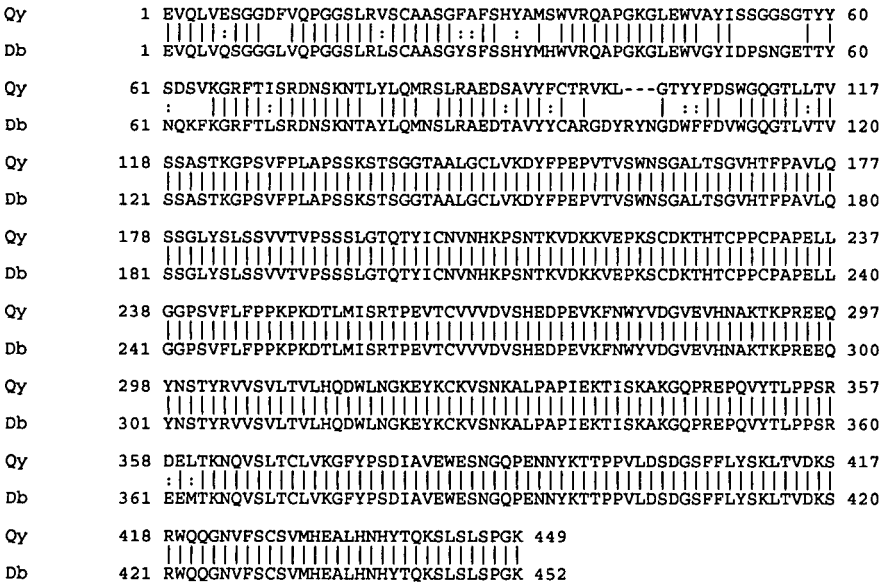
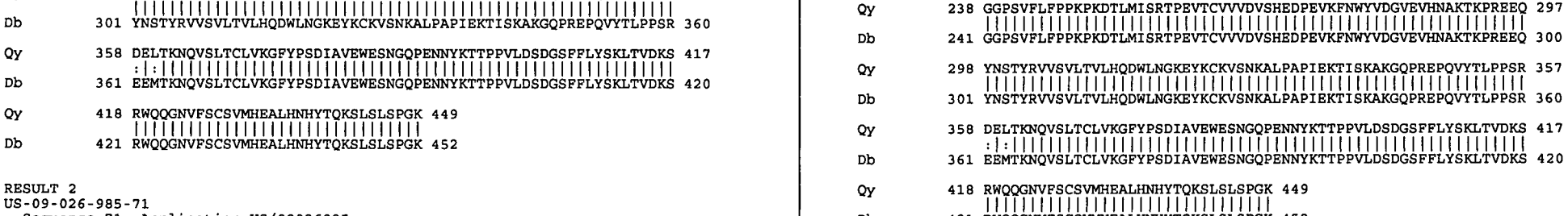


RESULT 2
US-09-026-985-71
; Sequence 71, Application US/09026985
; Patent No. 6133426
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/026,985
; FILING DATE: 20-Feb-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R3-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear

US-09-026-985-71

Query Match 71.5%; Score 2194.5; DB 3; Length 452;
Best Local Similarity 90.9%; Pred. No. 2.3e-161;
Matches 411; Conservative 14; Mismatches 24; Indels 3; Gaps 1;



RESULT 3
US-09-121-952A-71
; Sequence 71, Application US/09121952A
; Patent No. 6458355
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
; TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/121,952A
; FILING DATE: 24-Jul-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/074330
; FILING DATE: 22-JAN-1998
; PRIOR APPLICATION DATA:

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;      APPLICATION NUMBER:  60/075467
;      FILING DATE:  20-FEB-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  P1085R4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-5530
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  71:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  452 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-09-121-952A-71

  Query Match            71.5%;  Score 2194.5;  DB 4;  Length 452;
  Best Local Similarity  90.9%;  Pred. No. 2.3e-161;
  Matches  411;  Conservative   14;  Mismatches   24;  Indels    3;  Gaps    1;

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              |||||:|||  ||||||||:||||||::|| : | ||||||||||||| ||      | |
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Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKL---GTYYFDSWGQGTLLTV 117
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Qy        118 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 180

Qy        178 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 237
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Qy        238 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297
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Db        421 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 452


RESULT 4
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; Sequence 71, Application US/09234340A
; Patent No. 6468532
;  GENERAL INFORMATION:
;    APPLICANT:  Genentech, Inc., Hsei, Vanessa
;    APPLICANT:  Koumenis, Iphigenia
;    APPLICANT:  Leong, Steven R.
;    APPLICANT:  Presta, Leonard G.
;    APPLICANT:  Shahrokh, Zahra
;    APPLICANT:  Zapata, Gerardo A.
;    TITLE OF INVENTION:  METHODS OF TREATING INFLAMMATORY DISEASES
;    TITLE OF INVENTION:  WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
;    NUMBER OF SEQUENCES:  72
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/234,340A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/121,952
;      FILING DATE:  24-Jul-1998
;      APPLICATION NUMBER:  60/074330
;      FILING DATE:  22-JAN-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/075467
;      FILING DATE:  20-FEB-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  P1085R4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-5530
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  71:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  452 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-09-234-340A-71

  Query Match            71.5%;  Score 2194.5;  DB 4;  Length 452;
  Best Local Similarity  90.9%;  Pred. No. 2.3e-161;
  Matches  411;  Conservative   14;  Mismatches   24;  Indels    3;  Gaps    1;

Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60
              |||||:|||  ||||||||:||||||::|| : | ||||||||||||| ||      | |
Db          1 EVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMHWVRQAPGKGLEWVGYIDPSNGETTY 60

Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKL---GTYYFDSWGQGTLLTV 117
              :  |||||:|||||||| |||| ||||||:|||:| |      | ::|| ||||||:||
Db         61 NQKFKGRFTLSRDNSKNTAYLQMNSLRAEDTAVYYCARGDYRYNGDWFFDVWGQGTLVTV 120

Qy        118 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 180

Qy        178 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 240

Qy        238 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 300

Qy        298 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 360

Qy        358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 417
              :|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 420

Qy        418 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              ||||||||||||||||||||||||||||||||
Db        421 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 452


RESULT 5
US-08-157-101A-7
; Sequence 7, Application US/08157101A
; Patent No. 5808032
```

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;  GENERAL INFORMATION:
;    APPLICANT:  KURIHARA, TATSUYA
;    APPLICANT:  MATSUKURA, SHIGEKAZU
;    APPLICANT:  TSURUOKA, NOBUO
;    APPLICANT:  ARIMA, KENJI
;    APPLICANT:  NISHIHARA, TATSURO
;    TITLE OF INVENTION:  ANTI-HBs ANTIBODY GENES AND EXPRESSION
;    TITLE OF INVENTION:  PLASMIDS THEREFOR
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PILLSBURY, MADISON & SUTRO
;      STREET:  1100 NEW YORK AVENUE, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/157,101A
;      FILING DATE:  05-APR-1994
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  TITUS, MARLANA K
;      REGISTRATION NUMBER:  35843
;      REFERENCE/DOCKET NUMBER:  9437/204199
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-861-3711
;      TELEFAX:  202-822-0944
;      TELEX:  6714627 CUCH
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  459 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-157-101A-7

  Query Match             71.5%;  Score 2194.5;  DB 1;  Length 459;
  Best Local Similarity   91.8%;  Pred. No. 2.3e-161;
  Matches  413;  Conservative   15;  Mismatches   21;  Indels    1;  Gaps    1;

Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60
              :||||||||  |||| |||:|||||| ||  :| ||||||||||||| |   |:  :|
Db         10 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSNSMHWVRQAPGKGLEWVAVILYDGNHKFY 69

Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVK-LGTYYFDSWGQGTLLTVSS 119
              :|||||||||||||||||:::||: ||: ||:| | :  | : |||||||||:||||
Db         70 ADSVKGRFTISRDNSKNTLYLEVKSLQTEDTGVYYCIRDQTYGVHRFDSWGQGTLVTVSS 129

Qy        120 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        130 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALASGVHTFPAVLQSS 189

Qy        180 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 249

Qy        240 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 309

Qy        300 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 369

Qy        360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 419
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 429

Qy        420 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||||||||||||||
Db        430 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 459


RESULT 6
US-08-466-151-8
; Sequence 8, Application US/08466151
; Patent No. 6037453
;  GENERAL INFORMATION:
;    APPLICANT:  Jardieu, Paula M.
;    APPLICANT:  Presta, Leonard G.
;    TITLE OF INVENTION:  Immunoglobulin Variants
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/466,151
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/466163
;      FILING DATE:  06-Jun-1995
;      APPLICATION NUMBER:  08/405617
;      FILING DATE:  15-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/185899
;      FILING DATE:  26-JAN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/879495
;      FILING DATE:  07-MAY-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/744768
;      FILING DATE:  14-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Svoboda, Craig G.
;      REGISTRATION NUMBER:  39,044
;      REFERENCE/DOCKET NUMBER:  P0718P2C1D1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-1489
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  453 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-466-151-8

  Query Match             70.6%;  Score 2169;  DB 3;  Length 453;
  Best Local Similarity   91.0%;  Pred. No. 2.1e-159;
  Matches  413;  Conservative   16;  Mismatches   19;  Indels    6;  Gaps    4;

Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAF-SHYAMSWVRQAPGKGLEWVAYISSGGSGTY 59
              |||||||||  ||||||||:||| ||::  | |: :|:|||||||||||| |:  || |
Db          1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGS-TN 59

Qy         60 YSDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVK--LGTYYFDSWGQGTLLTV 117
              |:||||||||||:|||| |||| |||||:|||:| |      | ::|  |||||:||
Db         60 YADSVKGRFTISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGTLVTV 119

Qy        118 SSAST--KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 175
              |||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        120 SSASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 179

Qy        176 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE 239

Qy        236 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 299

Qy        296 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 359

Qy        356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 415
              ||:|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 419

Qy        416 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||||||||||||||||||
Db        420 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 453


RESULT 7
US-08-466-163B-8
; Sequence 8, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
;  APPLICANT: Jardieu, Paula M.
;  APPLICANT:  Presta, Leonard G.
;  TITLE OF INVENTION: Immunoglobulin Variants
;  FILE REFERENCE: P0718P2C1D1
;  CURRENT APPLICATION NUMBER: US/08/466,163B
;  CURRENT FILING DATE:  1995-06-06
;  PRIOR APPLICATION NUMBER: US 08/405,617
;  PRIOR FILING DATE: 1995-03-15
;  PRIOR APPLICATION NUMBER: US 08/185,899
;  PRIOR FILING DATE: 1994-01-26
;  PRIOR APPLICATION NUMBER: US 07/879,495
;  PRIOR FILING DATE: 1992-05-07
;  PRIOR APPLICATION NUMBER: US 07/744,768
;  PRIOR FILING DATE: 1991-08-14
;  NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 8
;   LENGTH: 453
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: humanized maell, version 1 heavy chain
US-08-466-163B-8

  Query Match           70.6%;  Score 2169;  DB 3;  Length 453;
  Best Local Similarity   91.0%;  Pred. No. 2.1e-159;
  Matches  413;  Conservative   16;  Mismatches   19;  Indels    6;  Gaps    4;

Qy      -       1 EVQLVESGGDFVQPGGSLRVSCAASGFAF-SHYAMSWVRQAPGKGLEWVAYISSGGSGTY 59
                  |||||||||  ||||||||:||| ||::  | |: :|:|||||||||||| |:  || |
Db              1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGS-TN 59

Qy         60 YSDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVK--LGTYYFDSWGQGTLLTV 117
              |:||||||||||||:|||| |||| |||||:|||:| |      | ::|  ||||||:||
Db         60 YADSVKGRFTISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGTLVTV 119

Qy        118 SSAST--KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 175
              |||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 SSASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 179

Qy        176 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE 239

Qy        236 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 299

Qy        296 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 359

Qy        356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 415
              ||:|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 419

Qy        416 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||||||||||||||||||
Db        420 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 453


RESULT 8
US-09-802-096-8
; Sequence 8, Application US/09802096
; Patent No. 6685939
; GENERAL INFORMATION:
;  APPLICANT:  Jardieu, Paula M.
;  APPLICANT:  Presta, Leonard G.
;  TITLE OF INVENTION:  Method of Preventing the Onset of Allergic Disorders (as amende
;  FILE REFERENCE:  P0718P2C3US
;  CURRENT APPLICATION NUMBER: US/09/802,096
;  CURRENT FILING DATE:  2001-03-08
;  PRIOR APPLICATION NUMBER:  US 08/405,617
;  PRIOR FILING DATE:  1995-03-15
;  PRIOR APPLICATION NUMBER:  US 08/185,899
;  PRIOR FILING DATE:  1994-01-26
;  PRIOR APPLICATION NUMBER:  PCT/US92/06860
;  PRIOR FILING DATE:  1992-08-14
;  PRIOR APPLICATION NUMBER:  US 07/879,495
;  PRIOR FILING DATE:  1992-05-07
;  PRIOR APPLICATION NUMBER:  US 07/744,768
;  PRIOR FILING DATE:  1991-08-14
;  NUMBER OF SEQ ID NOS:  64
; SEQ ID NO 8
;   LENGTH: 453
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: humanized maell, version 1 heavy chain
US-09-802-096-8

  Query Match           70.6%;  Score 2169;  DB 4;  Length 453;
  Best Local Similarity   91.0%;  Pred. No. 2.1e-159;
  Matches  413;  Conservative   16;  Mismatches   19;  Indels    6;  Gaps    4;

Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAF-SHYAMSWVRQAPGKGLEWVAYISSGGSGTY 59
              |||||||||  ||||||||:||| ||::  | |: :|:|||||||||||| |:  || |
Db          1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGS-TN 59

Qy         60 YSDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVK--LGTYYFDSWGQGTLLTV 117
              |:||||||||||||:|||| |||| |||||:|||:| |      | ::|  ||||||:||
Db         60 YADSVKGRFTISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGTLVTV 119

Qy        118 SSAST--KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 175
              |||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 SSASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 179

Qy        176 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE 239

Qy        236 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 299

Qy        296 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 359
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Qy        356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 415
              ||:|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 419

Qy        416 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||||||||||||||||||
Db        420 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 453


RESULT 9
US-09-802-077-8
; Sequence 8, Application US/09802077
; Patent No. 6699472
; GENERAL INFORMATION:
;  APPLICANT: Jardieu, Paula M.
;  APPLICANT:  Presta, Leonard G.
;  TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
;  FILE REFERENCE: P0718P2C2US
;  CURRENT APPLICATION NUMBER: US/09/802,077
;  CURRENT FILING DATE:  2001-03-08
;  PRIOR APPLICATION NUMBER: US 08/405,617
;  PRIOR FILING DATE: 1995-03-15
;  PRIOR APPLICATION NUMBER: US 08/185,899
;  PRIOR FILING DATE: 1994-01-26
;  PRIOR APPLICATION NUMBER: PCT/US92/06860
;  PRIOR FILING DATE: 1992-08-14
;  PRIOR APPLICATION NUMBER: US 07/879,495
;  PRIOR FILING DATE: 1992-05-07
;  PRIOR APPLICATION NUMBER: US 07/744,768
;  PRIOR FILING DATE: 1991-08-14
;  NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 8
;   LENGTH: 453
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: humanized maell, version 1 heavy chain
US-09-802-077-8

  Query Match             70.6%;  Score 2169;  DB 4;  Length 453;
  Best Local Similarity   91.0%;  Pred. No. 2.1e-159;
  Matches  413;  Conservative   16;  Mismatches   19;  Indels    6;  Gaps    4;

Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAF-SHYAMSWVRQAPGKGLEWVAYISSGGSGTY 59
              |||||||||  ||||||||:||| ||::  | |: :|:|||||||||||| |:  || |
Db          1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGS-TN 59

Qy         60 YSDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVK--LGTYYFDSWGQGTLLTV 117
              |:||||||||||:|||| |||| ||||||:|||:| |     | ::|  ||||||:||
Db         60 YADSVKGRFTISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGTLVTV 119

Qy        118 SSAST--KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 175
              |||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 SSASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 179

Qy        176 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE 239

Qy        236 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 299

Qy        296 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 359

Qy        356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 415
              ||:|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 419

Qy        416 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||||||||||||||||||
Db        420 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 453


RESULT 10
US-08-887-352B-14
; Sequence 14, Application US/08887352B
; Patent No. 5994511
;  GENERAL INFORMATION:
;    APPLICANT:  Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
;    TITLE OF INVENTION:  Improved Anti-IgE Antibodies and Method of
;    TITLE OF INVENTION:  Improving Polypeptides
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/887,352B
;      FILING DATE:  03-Jul-1997
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Svoboda, Craig G.
;      REGISTRATION NUMBER:  39,044
;      REFERENCE/DOCKET NUMBER:  P1123
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-1489
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  451 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-887-352B-14

  Query Match             70.6%;  Score 2167;  DB 2;  Length 451;
  Best Local Similarity   90.9%;  Pred. No. 3e-159;
  Matches  411;  Conservative   16;  Mismatches   21;  Indels    4;  Gaps    3;

Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAF-SHYAMSWVRQAPGKGLEWVAYISSGGSGTY 59
              |||||||||  ||||||||:||| ||::  | |: :|:|||||||||||| |:  || |
Db          1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGS-TN 59

Qy         60 YSDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVK--LGTYYFDSWGQGTLLTV 117
              |: ||||| |||||:|||| |||| ||||||:|||:| |     | ::|  ||||||:||
Db         60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGTLVTV 119

Qy        118 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 179

Qy        178 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 239

Qy        238 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 299

Qy        298 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 359

Qy        358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 417
              :|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 419
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```
Qy        418 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              ||||||||||||||||||||||||||||||||
Db        420 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451
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RESULT 11
US-08-887-352B-16
; Sequence 16, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-16

Query Match 70.6%; Score 2167; DB 2; Length 451;
Best Local Similarity 90.9%; Pred. No. 3e-159;
Matches 411; Conservative 16; Mismatches 21; Indels 4; Gaps 3;

```
Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAF-SHYAMSWVRQAPGKGLEWVAYISSGGSGTY 59
              |||||||||  ||||||||:||| ||::  | |: :|:||||||||||||| |:  || |
Db          1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGS-TN 59

Qy         60 YSDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVK--LGTYYFDSWGQGTLLTV 117
              |: ||||| ||||||:|||| |||| ||||||:|||:| |      | ::|  ||||||:||
Db         60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGTLVTV 119

Qy        118 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 179

Qy        178 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 239

Qy        238 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 299

Qy        298 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 359
```

```
Qy        358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 417
              :|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 419

Qy        418 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              ||||||||||||||||||||||||||||||||
Db        420 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451
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RESULT 12
US-08-466-151-65
; Sequence 65, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-466-151-65

Query Match 70.6%; Score 2167; DB 3; Length 451;
Best Local Similarity 90.9%; Pred. No. 3e-159;
Matches 411; Conservative 16; Mismatches 21; Indels 4; Gaps 3;

```
Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAF-SHYAMSWVRQAPGKGLEWVAYISSGGSGTY 59
              |||||||||  ||||||||:||| ||::  | |: :|:||||||||||||| |:  || |
Db          1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGS-TN 59

Qy         60 YSDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVK--LGTYYFDSWGQGTLLTV 117
              |: ||||| ||||||:|||| |||| ||||||:|||:| |      | ::|  ||||||:||
Db         60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGTLVTV 119
```

```
Qy        118 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 179

Qy        178 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 239

Qy        238 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 299

Qy        298 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 359

Qy        358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 417
              :|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 419

Qy        418 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              ||||||||||||||||||||||||||||||||
Db        420 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451
```

RESULT 13
US-09-109-207C-14
; Sequence 14, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-14

Query Match 70.6%; Score 2167; DB 3; Length 451;
Best Local Similarity 90.9%; Pred. No. 3e-159;
Matches 411; Conservative 16; Mismatches 21; Indels 4; Gaps 3;

```
Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAF-SHYAMSWVRQAPGKGLEWVAYISSGGSGTY 59
              |||||||||  ||||||||:||| ||::  | |: :|:|||||||||||| |:  || |
Db          1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGS-TN 59

Qy         60 YSDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVK--LGTYYFDSWGQGTLLTV 117
              |: ||||| |||||:|||| |||| |||||:|||:| |      | ::|  ||||||:||
Db         60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGTLVTV 119

Qy        118 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 179

Qy        178 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 239

Qy        238 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 299

Qy        298 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 359

Qy        358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 417
              :|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 419

Qy        418 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              ||||||||||||||||||||||||||||||||
Db        420 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451
```

RESULT 14
US-09-109-207C-16
; Sequence 16, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 16
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-16

Query Match 70.6%; Score 2167; DB 3; Length 451;
Best Local Similarity 90.9%; Pred. No. 3e-159;
Matches 411; Conservative 16; Mismatches 21; Indels 4; Gaps 3;

```
Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAF-SHYAMSWVRQAPGKGLEWVAYISSGGSGTY 59
              |||||||||  ||||||||:||| ||::  | |: :|:|||||||||||| |:  || |
Db          1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGS-TN 59

Qy         60 YSDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVK--LGTYYFDSWGQGTLLTV 117
              |: ||||| |||||:|||| |||| |||||:|||:| |      | ::|  ||||||:||
Db         60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGTLVTV 119

Qy        118 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 179

Qy        178 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 239

Qy        238 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 299

Qy        298 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 359

Qy        358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 417
              :|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 419

Qy        418 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              ||||||||||||||||||||||||||||||||
Db        420 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451
```

```
RESULT 15
US-09-296-005-14
; Sequence 14, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
;  APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
;  TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
;  FILE REFERENCE: P1123C1r
;  CURRENT APPLICATION NUMBER: US/09/296,005
;  CURRENT FILING DATE: 1999-04-21
;  EARLIER APPLICATION NUMBER: US 08/887,352
;  EARLIER FILING DATE: 1997-07-02
;  NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 14
;   LENGTH: 451
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   NAME/KEY: Artificial
;   LOCATION: 1-451
;   OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-296-005-14

  Query Match             70.6%;  Score 2167;  DB 3;  Length 451;
  Best Local Similarity   90.9%;  Pred. No. 3e-159;
  Matches  411;  Conservative   16;  Mismatches   21;  Indels    4;  Gaps    3;

Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAF-SHYAMSWVRQAPGKGLEWVAYISSGGSGTY 59
              |||||||||  ||||||||:||| ||::  | |: :|:||||||||||||| |:  || |
Db          1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGS-TN 59

Qy         60 YSDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVK--LGTYYFDSWGQGTLLTV 117
              |: ||||| |||||:|||| |||| ||||||:|||:| |     | ::|  ||||||:||
Db         60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGTLVTV 119

Qy        118 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 179

Qy        178 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 239

Qy        238 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 299

Qy        298 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 359

Qy        358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 417
              :|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 419

Qy        418 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
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Db        420 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451


Search completed: December 23, 2004, 19:07:50
Job time : 40.4376 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2004, 19:04:51 ; Search time 132.396 Seconds
(without alignments)
1578.640 Million cell updates/sec

Title: US-10-089-500-53
Perfect score: 3071
Sequence: 1 EVQLVESGGDFVQPGGSLRV.....IVEFLNRWITFCQSIISTLT 582

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1595201 seqs, 359116952 residues

Total number of hits satisfying chosen parameters: 1595201

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2750.5	89.6	579	14	US-10-138-727A-41	Sequence 41, Appl
2	2750.5	89.6	579	14	US-10-310-719-32	Sequence 32, Appl
3	2719.5	88.6	575	17	US-10-737-208A-6	Sequence 6, Appli
4	2621	85.3	580	14	US-10-310-719-37	Sequence 37, Appl
5	2589	84.3	580	14	US-10-310-719-35	Sequence 35, Appl
6	2246.5	73.2	447	15	US-10-474-832-4	Sequence 4, Appli
7	2240.5	73.0	447	15	US-10-474-832-5	Sequence 5, Appli
8	2238.5	72.9	663	15	US-10-412-406-32	Sequence 32, Appl
9	2238.5	72.9	4852	15	US-10-412-406-33	Sequence 33, Appl
10	2236.5	72.8	447	15	US-10-474-832-6	Sequence 6, Appli
11	2234.5	72.8	445	14	US-10-320-231A-79	Sequence 79, Appl
12	2231.5	72.7	444	14	US-10-150-475A-6	Sequence 6, Appli
13	2231.5	72.7	444	16	US-10-704-522-6	Sequence 6, Appli
14	2231.5	72.7	444	16	US-10-645-215-6	Sequence 6, Appli
15	2226	72.5	449	9	US-09-736-371B-21	Sequence 21, Appl
16	2226	72.5	449	15	US-10-463-442-21	Sequence 21, Appl
17	2222.5	72.4	477	14	US-10-291-265-395	Sequence 395, App
18	2221.5	72.3	446	15	US-10-408-901-38	Sequence 38, Appl
19	2220	72.3	474	10	US-09-848-832-3	Sequence 3, Appli
20	2220	72.3	474	14	US-10-225-108A-3	Sequence 3, Appli
21	2220	72.3	474	15	US-10-461-148-1	Sequence 1, Appli
22	2216.5	72.2	442	15	US-10-226-435A-12	Sequence 12, Appl
23	2216.5	72.2	442	17	US-10-487-326-12	Sequence 12, Appl
24	2216.5	72.2	442	17	US-10-486-908-12	Sequence 12, Appl
25	2216	72.2	451	9	US-09-822-698A-26	Sequence 26, Appl
26	2212	72.0	445	15	US-10-408-901-34	Sequence 34, Appl
27	2209.5	71.9	442	17	US-10-487-322-12	Sequence 12, Appl
28	2209.5	71.9	442	17	US-10-487-326-21	Sequence 21, Appl
29	2209.5	71.9	442	17	US-10-486-908-16	Sequence 16, Appl
30	2202.5	71.7	446	15	US-10-408-901-46	Sequence 46, Appl
31	2202.5	71.7	469	17	US-10-858-186-14	Sequence 14, Appl
32	2198.5	71.6	469	15	US-10-656-769-26	Sequence 26, Appl
33	2195	71.5	445	15	US-10-408-901-42	Sequence 42, Appl
34	2194.5	71.5	452	10	US-09-726-258-71	Sequence 71, Appl
35	2192.5	71.4	469	15	US-10-656-769-20	Sequence 20, Appl
36	2191	71.3	474	15	US-10-108-260A-4640	Sequence 4640, Ap
37	2191	71.3	713	16	US-10-679-620-64	Sequence 64, Appl
38	2191	71.3	715	16	US-10-679-620-62	Sequence 62, Appl
39	2190.5	71.3	452	17	US-10-818-765-4	Sequence 4, Appli
40	2186.5	71.2	446	15	US-10-408-901-30	Sequence 30, Appl
41	2185.5	71.2	446	15	US-10-408-901-50	Sequence 50, Appl
42	2184.5	71.1	447	16	US-10-379-392-116	Sequence 116, App
43	2183.5	71.1	447	16	US-10-379-392-117	Sequence 117, App
44	2181	71.0	451	14	US-10-423-299-4	Sequence 4, Appli
45	2180.5	71.0	447	16	US-10-379-392-119	Sequence 119, App

ALIGNMENTS

RESULT 1
US-10-138-727A-41
; Sequence 41, Application US/10138727A
; Publication No. US20030157054A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Susan
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/10/138,727A
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 41
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: heavy chain-IL2
US-10-138-727A-41

Query Match 89.6%; Score 2750.5; DB 14; Length 579;
Best Local Similarity 88.5%; Pred. No. 8.2e-166;
Matches 516; Conservative 32; Mismatches 30; Indels 5; Gaps 2;

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Db          1 QIQLVQSGAEVKKPGETVKISCKASGYTFTNYGMNWVKQTPGKGLKWMGWINTYTGEPTY 60

Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTR-VKLGTYYFDSWGQGTLLTVSS 119
              :| |||| | : | :| :||: :||:||:| ||| | :  | |    ||||| :||||
Db         61 ADDFKGRFAFSLETSTSTAFLQINNLRSEDTATYFCVRFISKGDY----WGQGTSVTVSS 116
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Qy        120 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
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Db        117 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 176

Qy        180 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 239
              ||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||||||
Db        177 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGG 236

Qy        240 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        237 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 296

Qy        300 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359
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Db        297 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE 356

Qy        360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 419
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        420 QQGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMILNGINN 479
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Db        417 QQGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMILNGINN 476

Qy        480 YKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNIN 539
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        477 YKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNIN 536

Qy        540 VIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 582
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Db        537 VIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 579
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RESULT 2
US-10-310-719-32
; Sequence 32, Application US/10310719
; Publication No. US20030166163A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Immunocytokines With Modulated Selectivity
; FILE REFERENCE: LEX-020
; CURRENT APPLICATION NUMBER: US/10/310,719
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,113
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/371,966
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: dI-KS-ala IL2 (D20T) heavy chain fused to IL-2 variant
US-10-310-719-32

Query Match 89.6%; Score 2750.5; DB 14; Length 579;
Best Local Similarity 88.5%; Pred. No. 8.2e-166;
Matches 516; Conservative 32; Mismatches 30; Indels 5; Gaps 2;

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              ::|||:|| :  :|| |:::|| |||: |::| |:|||||||||:|: :|::      |
Db          1 QIQLVQSGPELKKPGSSVKISCKASGYTFTNYGMNWVRQAPGKGLKWMGWINTYTGEPTY 60

Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTR-VKLGTYYFDSWGQGTLLTVSS 119
              :|  ||||||: : | :|||||: :||:||:| ||| | :  | |    ||||| :||||
Db         61 ADDFKGRFTITAETSTSTLYLQLNNLRSEDTATYFCVRFISKGDY----WGQGTTVTVSS 116

Qy        120 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
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Db        117 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 176
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Db        177 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGG 236

Qy        240 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299
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Db        237 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 296

Qy        300 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359
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Db        297 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE 356

Qy        360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 419
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Db        357 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 416

Qy        420 QQGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMILNGINN 479
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Qy        480 YKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNIN 539
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Db        477 YKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNIN 536

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RESULT 3
US-10-737-208A-6
; Sequence 6, Application US/10737208A
; Publication No. US20040203100A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen D.
; APPLICANT: Lo, Kin-Ming
; TITLE OF INVENTION: IMMUNOCYTOKINE SEQUENCES AND USES THEREOF
; FILE REFERENCE: LEX-023
; CURRENT APPLICATION NUMBER: US/10/737,208A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 60/433,945
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized Immunoglobulin Heavy Chain-IL-2
US-10-737-208A-6

Query Match 88.6%; Score 2719.5; DB 17; Length 575;
Best Local Similarity 89.0%; Pred. No. 7.4e-164;
Matches 518; Conservative 24; Mismatches 33; Indels 7; Gaps 3;

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Db          1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY 60

Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYFDSWGQGTLLTVSSA 120
              :   ||| |:: | | :| |: ::|||:||:|||:|     |  |   ||||| :|||||
Db         61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDTAVYYCVS---GMEY---WGQGTSVTVSSA 114

Qy        121 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 174

Qy        181 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 240
              |||||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||
Db        175 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGP 234

Qy        241 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300
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Qy        359 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 418
              |:|||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db        357 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSR 416

Qy        419 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMILNGIN 478
              |||||||||||||||||||||| : :|| |||||||||||||||||| |||||||||
Db        417 WQQGNVFSCSVMHEALHNHYTQKSATATPGAAPTSSSTKKTQLQLEHLLLTLQMILNGIN 476

Qy        479 NYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNI 538
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        477 NYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNI 536

Qy        539 NVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 582
              |||||||||||||||||||||||||||||||||||||||||||
Db        537 NVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 580
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RESULT 6
US-10-474-832-4
; Sequence 4, Application US/10474832
; Publication No. US20040081651A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: ANTIBODIES TO VLA-1
; FILE REFERENCE: A101 PCT
; CURRENT APPLICATION NUMBER: US/10/474,832
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/283,794
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/303,689
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: polypeptide
US-10-474-832-4

Query Match 73.2%; Score 2246.5; DB 15; Length 447;
Best Local Similarity 95.1%; Pred. No. 4.8e-134;
Matches 426; Conservative 4; Mismatches 17; Indels 1; Gaps 1;

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Db          1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSRYTMSWVRQAPGKGLEWVATISGGGH-TYY 59

Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYFDSWGQGTLLTVSSA 120
              |||||||||||||||||||| ||||||:|||:|||      ||| ||||||:|||||
Db         60 LDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRGFGDGGYFDVWGQGTLVTVSSA 119

Qy        121 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 179

Qy        181 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 239

Qy        241 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 299

Qy        301 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 359

Qy        361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 419

Qy        421 QGNVFSCSVMHEALHNHYTQKSLSLSPG 448
              ||||||||||||||||||||||||||||
Db        420 QGNVFSCSVMHEALHNHYTQKSLSLSPG 447
```

RESULT 7
US-10-474-832-5
; Sequence 5, Application US/10474832
; Publication No. US20040081651A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: ANTIBODIES TO VLA-1
; FILE REFERENCE: A101 PCT
; CURRENT APPLICATION NUMBER: US/10/474,832
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/283,794
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/303,689
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: polypeptide
US-10-474-832-5

Query Match 73.0%; Score 2240.5; DB 15; Length 447;
Best Local Similarity 94.9%; Pred. No. 1.1e-133;
Matches 425; Conservative 4; Mismatches 18; Indels 1; Gaps 1;

```
Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60
              |||||||||  ||||||||:||||||| || | ||||||||||||||| || ||  |||
Db          1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSRYTMSWVRQAPGKGLEWVATISGGGH-TYY 59

Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYFDSWGQGTLLTVSSA 120
              |||||||||||||||||||| ||||||:|||:|||      ||| ||||||:|||||
Db         60 LDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRGFGDGGYFDVWGQGTLVTVSSA 119

Qy        121 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 179

Qy        181 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 239

Qy        241 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        240 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYQS 299

Qy        301 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 359

Qy        361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 419

Qy        421 QGNVFSCSVMHEALHNHYTQKSLSLSPG 448
              ||||||||||||||||||||||||||||
Db        420 QGNVFSCSVMHEALHNHYTQKSLSLSPG 447
```

RESULT 8
US-10-412-406-32
; Sequence 32, Application US/10412406
; Publication No. US20040058394A1

; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; APPLICANT: GARBER, Ellen
; APPLICANT: LYNE, Paul
; APPLICANT: SALDHANA, Jose W.
; TITLE OF INVENTION: HUMANIZED ANTI-LT-BETA-R ANTIBODIES
; FILE REFERENCE: BINA100CN
; CURRENT APPLICATION NUMBER: US/10/412,406
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: 60/240,285
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/275,289
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/299,987
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: PCT/US01/32140
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-412-406-32

Query Match 72.9%; Score 2238.5; DB 15; Length 663;
Best Local Similarity 94.0%; Pred. No. 2.4e-133;
Matches 422; Conservative 8; Mismatches 18; Indels 1; Gaps 1;

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Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60
              |||||||||  |:||||||:||||||| || | | | ||||||||||||| || ||| |||
Db        215 EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMYWFRQAPGKGLEWVATISDGGSYTYY 274

Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGT-YYFDSWGQGTLLTVSS 119
                |||||||||||||:||:|||| ||||||:|||:| | : |  |||| ||||| :||||
Db        275 PDSVKGRFTISRDNAKNSLYLQMSSLRAEDTAVYYCAREENGNFYYFDYWGQGTTVTVSS 334

Qy        120 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        335 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 394

Qy        180 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        395 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 454

Qy        240 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        455 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 514

Qy        300 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        515 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 574

Qy        360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 419
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        575 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 634

Qy        420 QQGNVFSCSVMHEALHNHYTQKSLSLSPG 448
              |||||||||||||||||||||||||||||
Db        635 QQGNVFSCSVMHEALHNHYTQKSLSLSPG 663
```

RESULT 9
US-10-412-406-33
; Sequence 33, Application US/10412406
; Publication No. US20040058394A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; APPLICANT: GARBER, Ellen
; APPLICANT: LYNE, Paul
; APPLICANT: SALDHANA, Jose W.
; TITLE OF INVENTION: HUMANIZED ANTI-LT-BETA-R ANTIBODIES
; FILE REFERENCE: BINA100CN
; CURRENT APPLICATION NUMBER: US/10/412,406
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: 60/240,285
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/275,289
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/299,987
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: PCT/US01/32140
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 4852
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-412-406-33

Query Match 72.9%; Score 2238.5; DB 15; Length 4852;
Best Local Similarity 94.0%; Pred. No. 2.5e-132;
Matches 422; Conservative 8; Mismatches 18; Indels 1; Gaps 1;

```
Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60
              |||||||||  |:||||||:||||||| || | | | ||||||||||||| || ||| |||
Db       4404 EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMYWFRQAPGKGLEWVATISDGGSYTYY 4463

Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGT-YYFDSWGQGTLLTVSS 119
                |||||||||||||:||:|||| ||||||:|||:| | : |  |||| ||||| :||||
Db       4464 PDSVKGRFTISRDNAKNSLYLQMSSLRAEDTAVYYCAREENGNFYYFDYWGQGTTVTVSS 4523

Qy        120 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4524 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 4583

Qy        180 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4584 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 4643

Qy        240 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4644 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 4703

Qy        300 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4704 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 4763

Qy        360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 419
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4764 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 4823

Qy        420 QQGNVFSCSVMHEALHNHYTQKSLSLSPG 448
              |||||||||||||||||||||||||||||
Db       4824 QQGNVFSCSVMHEALHNHYTQKSLSLSPG 4852
```

RESULT 10
US-10-474-832-6
; Sequence 6, Application US/10474832
; Publication No. US20040081651A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: ANTIBODIES TO VLA-1
; FILE REFERENCE: A101 PCT
; CURRENT APPLICATION NUMBER: US/10/474,832
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/283,794
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/303,689
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 447

```
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: polypeptide
US-10-474-832-6

  Query Match             72.8%;  Score 2236.5;  DB 15;  Length 447;
  Best Local Similarity   94.6%;  Pred. No. 2.1e-133;
  Matches  424;  Conservative    4;  Mismatches   19;  Indels    1;  Gaps    1;

Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60
              |||||||||  ||||||||:|||||||  ||  |  ||||||||||||||||  ||  ||   |||
Db          1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSRYTMSWVRQAPGKGLEWVATISGGGH-TYY 59

Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYFDSWGQGTLLTVSSA 120
               |||||||||||||||||||||| ||||||:|||:|||      ||| ||||||:|||||
Db         60 LDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRGFGDGGYFDVWGQGTLVTVSSA 119

Qy        121 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 179

Qy        181 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        180 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGP 239

Qy        241 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 299

Qy        301 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 359

Qy        361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 419

Qy        421 QGNVFSCSVMHEALHNHYTQKSLSLSPG 448
              ||||||||||||||||||||||||||||
Db        420 QGNVFSCSVMHEALHNHYTQKSLSLSPG 447


RESULT 11
US-10-320-231A-79
; Sequence 79, Application US/10320231A
; Publication No. US20030194405A1
; GENERAL INFORMATION:
;  APPLICANT: Neben, Steven
;  APPLICANT:  Takeuchi, Toshihiko
;  APPLICANT:  Tomkinson, Adrian
;  TITLE OF INVENTION: Antibody Inhibiting Stem Cell Factor Activity And Use For
;  TITLE OF INVENTION:  Treatment Of Asthma
;  FILE REFERENCE: 7430*163
;  CURRENT APPLICATION NUMBER: US/10/320,231A
;  CURRENT FILING DATE:  2002-12-19
;  PRIOR APPLICATION NUMBER: US 60/342,174
;  PRIOR FILING DATE: 2001-12-17
;  NUMBER OF SEQ ID NOS: 85
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 79
;   LENGTH: 445
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: synthetic sequence
US-10-320-231A-79

  Query Match             72.8%;  Score 2234.5;  DB 14;  Length 445;
  Best Local Similarity   94.4%;  Pred. No. 2.7e-133;
  Matches  421;  Conservative    7;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          4 LVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYYSDS 63
              ||||||  ||||||||:|||||||  ||  ||||||||||||||||: ||  |  |||:||
Db          1 LVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADS 60

Qy         64 VKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYFDSWGQGTLLTVSSASTK 123
               ||||||||||||||||||| ||||||:|||:| |      :|| ||||||:|||||||
Db         61 VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRDFFA-HFDVWGQGTLVTVSSASTK 119

Qy        124 GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS 179

Qy        184 LSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVF 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 LSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVF 239

Qy        244 LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR 299

Qy        304 VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKN 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKN 359

Qy        364 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN 419

Qy        424 VFSCSVMHEALHNHYTQKSLSLSPGK 449
              ||||||||||||||||||||||||||
Db        420 VFSCSVMHEALHNHYTQKSLSLSPGK 445


RESULT 12
US-10-150-475A-6
; Sequence 6, Application US/10150475A
; Publication No. US20030103985A1
; GENERAL INFORMATION:
;  APPLICANT: Adolf, G. et al.
;  TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates
;  FILE REFERENCE: 1/1211
;  CURRENT APPLICATION NUMBER: US/10/150,475A
;  CURRENT FILING DATE:  2002-05-17
;  PRIOR APPLICATION NUMBER: US 60/307,451
;  PRIOR FILING DATE: 2001-07-24
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 444
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Humanised
;   OTHER INFORMATION: Murine Antibody BIWA 4 Heavy Chain SEQ ID NO: 6
US-10-150-475A-6

  Query Match             72.7%;  Score 2231.5;  DB 14;  Length 444;
  Best Local Similarity   93.8%;  Pred. No. 4.2e-133;
  Matches  421;  Conservative   10;  Mismatches   13;  Indels    5;  Gaps    1;

Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60
              |||||||||  |:|||||:|||||||  ||  | ||||||||||||||: ||||||  |||
Db          1 EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVSTISSGGSYTYY 60

Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYFDSWGQGTLLTVSSA 120
               ||:|||||||||:||:|||||  ||||||:|||:|  |   |     | ||:|||:|||||
Db         61 LDSIKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARQGL-----DYWGRGTLVTVSSA 115

Qy        121 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        116 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 175

Qy        181 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 240
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        176 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 235

Qy        241 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        236 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 295

Qy        301 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 355

Qy        361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        356 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 415

Qy        421 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
                ||||||||||||||||||||||||||||
Db        416 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 444


RESULT 13
US-10-704-522-6
; Sequence 6, Application US/10704522
; Publication No. US20040120949A1
; GENERAL INFORMATION:
;  APPLICANT: Adolf, Gunther
;  APPLICANT:  Baumann, Michael
;  APPLICANT:  Heider, Karl-Heinz
;  TITLE OF INVENTION: Compositions and methods for treating cancer using
;  TITLE OF INVENTION:  cytotoxic CD44 Antibody Immunoconjugates
;  FILE REFERENCE: 1/1414
;  CURRENT APPLICATION NUMBER: US/10/704,522
;  CURRENT FILING DATE:  2003-11-07
;  PRIOR APPLICATION NUMBER: US 60/429,516
;  PRIOR FILING DATE: 2002-11-27
;  PRIOR APPLICATION NUMBER: EP 02024881
;  PRIOR FILING DATE: 2002-11-08
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 444
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Heavy Chain
US-10-704-522-6

  Query Match             72.7%;  Score 2231.5;  DB 16;  Length 444;
  Best Local Similarity   93.8%;  Pred. No. 4.2e-133;
  Matches  421;  Conservative   10;  Mismatches   13;  Indels    5;  Gaps    1;

Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60
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Db          1 EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVSTISSGGSYTYY 60

Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYFDSWGQGTLLTVSSA 120
                ||:||||||||||:||:|||||  ||||||:|||:| |  |      | ||:|||:|||||
Db         61 LDSIKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARQGL-----DYWGRGTLVTVSSA 115

Qy        121 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        116 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 175

Qy        181 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        176 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 235

Qy        241 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300
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Db        236 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 295

Qy        301 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 355

Qy        361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        356 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 415

Qy        421 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
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Db        416 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 444


RESULT 14
US-10-645-215-6
; Sequence 6, Application US/10645215
; Publication No. US20040126379A1
; GENERAL INFORMATION:
;  APPLICANT: Adolf, Guenther
;  APPLICANT:  Baum, Anke
;  APPLICANT:  Heider, Karl-Heinz
;  TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
;  TITLE OF INVENTION:  Cytotoxic CD44 Antibody Immunoconjugates and
;  TITLE OF INVENTION:  Chemotherapeutic Agents
;  FILE REFERENCE: 1/1383
;  CURRENT APPLICATION NUMBER: US/10/645,215
;  CURRENT FILING DATE:  2003-08-21
;  PRIOR APPLICATION NUMBER: EP 02 018 686.2
;  PRIOR FILING DATE: August 21, 2002
;  PRIOR APPLICATION NUMBER: US 60/405,956
;  PRIOR FILING DATE: August 26, 2002
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 444
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Heavy Chain
US-10-645-215-6

  Query Match             72.7%;  Score 2231.5;  DB 16;  Length 444;
  Best Local Similarity   93.8%;  Pred. No. 4.2e-133;
  Matches  421;  Conservative   10;  Mismatches   13;  Indels    5;  Gaps    1;

Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60
              |||||||||  |:|||||:|||||||  || | |||||||||||||||: ||||||  |||
Db          1 EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVSTISSGGSYTYY 60

Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYFDSWGQGTLLTVSSA 120
                ||:||||||||||:||:|||||  ||||||:|||:| |  |      | ||:|||:|||||
Db         61 LDSIKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARQGL-----DYWGRGTLVTVSSA 115

Qy        121 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        181 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 240
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Qy        241 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300
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Qy        301 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360
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Db        296 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 355

Qy        361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        356 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 415

Qy        421 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
                ||||||||||||||||||||||||||||
Db        416 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 444
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Db        416 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 444


RESULT 15
US-09-736-371B-21
; Sequence 21, Application US/09736371B
; Patent No. US20020131968A1
; GENERAL INFORMATION:
;  APPLICANT: Waldmann, Herman
;  APPLICANT:  Frewin, Mark
;  TITLE OF INVENTION: AGLYCOSYLATED ANTIBODIES
;  FILE REFERENCE: Waldmann
;  CURRENT APPLICATION NUMBER: US/09/736,371B
;  CURRENT FILING DATE:  2002-04-25
;  PRIOR APPLICATION NUMBER: 9815909.8
;  PRIOR FILING DATE: 1998-07-21
;  PRIOR APPLICATION NUMBER: PCT/GB99/02380
;  PRIOR FILING DATE: 1999-07-21
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
;   LENGTH: 449
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-736-371B-21

  Query Match            72.5%;  Score 2226;  DB 9;  Length 449;
  Best Local Similarity  93.1%;  Pred. No. 9.5e-133;
  Matches  418;  Conservative   12;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60
              ||||:||||  ||||||||:|||||||  || : |:|||||||||||||: ||: |  |||
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Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYFDSWGQGTLLTVSSA 120
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Qy        121 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180
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Qy        241 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYAS 300

Qy        301 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360

Qy        361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 420

Qy        421 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||||||||||||||
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Search completed: December 23, 2004, 19:35:46
Job time : 134.396 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2004, 18:46:03 ; Search time 31.449 Seconds
(without alignments)
1780.604 Million cell updates/sec

Title: US-10-089-500-53
Perfect score: 3071
Sequence: 1 EVQLVESGGDFVQPGGSLRV.....IVEFLNRWITFCQSIISTLT 582

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1767	57.5	330	1	GHHU	Ig gamma-1 chain C
2	1630.5	53.1	377	2	A23511	Ig gamma-3 chain C
3	1628.5	53.0	377	2	A60764	Ig gamma-3 chain C
4	1604	52.2	326	1	G2HU	Ig gamma-2 chain C
5	1590.5	51.8	327	1	G4HU	Ig gamma-4 chain C
6	1508.5	49.1	444	2	PC4436	monoclonal antibod
7	1487	48.4	470	2	S22080	Ig heavy chain pre
8	1440.5	46.9	469	2	S37483	Ig gamma-2a chain
9	1437	46.8	446	2	S40295	Ig gamma-2a chain
10	1434	46.7	472	2	S31459	Ig gamma-1 chain -
11	1429	46.5	374	2	S69339	Ig heavy chain V r
12	1390	45.3	474	1	G2MS11	Ig gamma-2b chain
13	1367.5	44.5	475	2	S01321	Ig gamma-2b chain
14	1263	41.1	328	2	I47159	Ig gamma 2a chain
15	1260	41.0	255	4	S31866	Ig gamma-1 chain C
16	1257	40.9	328	2	I47160	Ig gamma 2b chain
17	1254	40.8	234	2	PT0207	Ig gamma chain C r
18	1231	40.1	328	2	I47158	Ig gamma 1 chain c
19	1230.5	40.1	323	1	GHRB	Ig gamma chain C r
20	1227	40.0	328	2	I47161	Ig gamma 3 chain c
21	1216.5	39.6	329	1	G2GP	Ig gamma-2 chain C
22	1161.5	37.8	308	2	C30554	Ig heavy chain C r
23	1152	37.5	326	2	PS0017	Ig gamma-1 chain C
24	1151	37.5	289	1	G3HUWI	Ig gamma-3 heavy c
25	1146.5	37.3	333	2	PS0018	Ig gamma-2b chain
26	1142	37.2	324	1	G1MS	Ig gamma-1 chain C
27	1141	37.2	329	1	G3MSC	Ig gamma-3 chain C
28	1139	37.1	393	1	G1MSM	Ig gamma-1 chain C
29	1130	36.8	398	1	G3MSM	Ig gamma-3 chain C
30	1126	36.7	330	1	G2MSA	Ig gamma-2a chain
31	1123.5	36.6	335	1	G2MSAB	Ig gamma-2a chain
32	1121	36.5	399	1	G2MSAM	Ig gamma-2a chain
33	1118.5	36.4	329	2	S00847	Ig gamma-2c chain
34	1112	36.2	322	2	PS0019	Ig gamma-2a chain
35	1102	35.9	548	2	S38864	Ig epsilon chain C
36	1092.5	35.6	327	2	S06611	Ig gamma-2 chain C
37	1082	35.2	405	1	G2MSBM	Ig gamma-2b chain
38	1066	34.7	277	2	I47162	Ig gamma 4 chain c
39	866.5	28.2	549	2	S04845	Ig heavy chain pre
40	856.5	27.9	249	2	S69340	Ig heavy chain VHI
41	820.5	26.7	241	2	S69131	Ig heavy chain (DO
42	817.5	26.6	572	2	B46529	Ig Y heavy chain (
43	810	26.4	218	2	A36040	Ig heavy chain V-I
44	792	25.8	220	2	A49444	Ig gamma-1 heavy c
45	750	24.4	246	2	S38950	Ig gamma chain - m

ALIGNMENTS

RESULT 1
GHHU
Ig gamma-1 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C;Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
R;Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A;Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A;Reference number: A93433; MUID:82274238; PMID:6287432
A;Accession: A93433
A;Molecule type: DNA
A;Residues: 1-330 <ELL>
A;Cross-references: UNIPROT:P01857; EMBL:Z17370
A;Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers,
A;Note: Lys-330 is removed after translation
R;Harris, L.J.
submitted to the EMBL Data Library, October 1992
A;Reference number: S33904
A;Accession: S36861
A;Molecule type: DNA
A;Residues: 2-330 <HAR>
A;Cross-references: EMBL:Z17370
R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
A;Reference number: S33887; MUID:83001943; PMID:6811139
A;Accession: S33887
A;Molecule type: DNA
A;Residues: 88-113;235-330 <TAK>
A;Cross-references: EMBL:Z17370
R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,
Biochemistry 9, 3161-3170, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seque
A;Reference number: A90563; MUID:71064024; PMID:5489771
A;Contents: myeloma protein Eu
A;Accession: B90563
A;Molecule type: protein
A;Residues: 1-96,'R',98-135 <CUN>
A;Note: this sequence has the G1m(3) marker, 97-Arg
R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequ
A;Reference number: A90564; MUID:71064025; PMID:5530842
A;Contents: Eu
A;Accession: A90564
A;Molecule type: protein
A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240,
A;Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met
R;Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A;Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),

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igen Primaerstruktur.
A;Reference number: A91668; MUID:77070269; PMID:826475
A;Contents: myeloma protein Nie
A;Accession: B91668
A;Molecule type: protein
A;Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',27
A;Note: this sequence has the G1m(17) and G1m(1) markers
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A;Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KOL
A;Reference number: A91723; MUID:83289131; PMID:6884994
A;Contents: myeloma protein KOL; disulfide bonds
A;Accession: A91723
A;Molecule type: protein
A;Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SCH
A;Note: this sequence has the G1m(3) and G1m(non-1) markers
R;Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A;Reference number: A90565; MUID:71064027; PMID:4923144
A;Contents: annotation; disulfide bonds
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enbromide cleavage products, and the disulfide bridges.
A;Reference number: A91667; MUID:77070267; PMID:1002129
A;Contents: annotation; disulfide bonds
C;Genetics:
A;Gene: GDB:IGHG1
A;Cross-references: GDB:120085; OMIM:147100
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 114/1; 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;137-206/Domain: immunoglobulin homology <IM2>
F;243-310/Domain: immunoglobulin homology <IM3>
F;27-83,144-204,250-308/Disulfide bonds: #status experimental
F;103/Disulfide bonds: interchain (to light chain) #status experimental
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental

  Query Match             57.5%;  Score 1767;  DB 1;  Length 330;
  Best Local Similarity   100.0%;  Pred. No. 5.9e-92;
  Matches  330;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        120 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy        180 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120

Qy        240 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299
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Db        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

Qy        300 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359
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Db        181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

Qy        360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 419
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Db        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300

Qy        420 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
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Db        301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
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RESULT 2
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C;Accession: A23511
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: co
A;Reference number: A23511; MUID:86148507; PMID:3081877
A;Accession: A23511
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
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A;Gene: GDB:IGHG3
A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
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C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

  Query Match             53.1%;  Score 1630.5;  DB 2;  Length 377;
  Best Local Similarity   82.0%;  Pred. No. 3e-84;
  Matches  309;  Conservative   10;  Mismatches   11;  Indels   47;  Gaps    1;

Qy        120 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
              |||||||||||||| |:|||||||||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy        180 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV---------------------- 217
              |||||||||||||||||||| |||||||||||||||:|
Db         61 GLYSLSSVVTVPSSSLGTQTYTCNVNHKPSNTKVDKRVELKTPLGDTTHTCPRCPEPKSC 120

Qy        218 -------------------------EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDT 252
                                      ||||||    || ||||||||||||||||||||||
Db        121 DTPPPCPRCPEPKSCDTPPPCPRCPEPKSCDTPPPCPRCPAPELLGGPSVFLFPPKPKDT 180

Qy        253 LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH 312
              |||||||||||||||||||||||:| ||||||||||||||||||:||||||||||
Db        181 LMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQYNSTFRVVSVLTVLH 240

Qy        313 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK 372
              |||||||||||||||||||||||||| ||||||||||||:|:||||||||||||
Db        241 QDWLNGKEYKCKVSNKALPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVK 300

Qy        373 GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE 432
              |||||||||||:||||||| ||||:||||||||||||||||||:||||||||
Db        301 GFYPSDIAVEWESSGQPENNYNTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHE 360

Qy        433 ALHNHYTQKSLSLSPGK 449
              |||| :||||||||||
Db        361 ALHNRFTQKSLSLSPGK 377
```

```
RESULT 3
A60764
Ig gamma-3 chain C region, form LAT - human
C;Species: Homo sapiens (man)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
C;Accession: A60764
R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 convert
A;Reference number: A60764; MUID:90007613; PMID:2571587
A;Accession: A60764
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: UNIPROT:Q8N4Y9
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
```

F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 53.0%; Score 1628.5; DB 2; Length 377;
Best Local Similarity 82.0%; Pred. No. 3.9e-84;
Matches 309; Conservative 10; Mismatches 11; Indels 47; Gaps 1;

```
Qy      120 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
            |||||||||||||| |:||||||||||||||||||||||||||||||||||||||||||||
Db        1 ASTKGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy      180 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV---------------------- 217
            |||||||||||||||||||| |||||||||||||:|
Db       61 GLYSLSSVVTVPSSSLGTQTYTCNVNHKPSNTKVDKRVELKTPLGDTTHTCPRCPEPKSC 120

Qy      218 ------------------------EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDT 252
                                     ||||||    || ||||||||||||||||||||||
Db      121 DTPPPCPRCPEPKSCDTPPPCPRCPEPKSCDTPPPCPRCPAPELLGGPSVFLFPPKPKDT 180

Qy      253 LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH 312
            |||||||||||||||||||||:| ||||||||||||||||||||:||||||||||
Db      181 LMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQYNSTFRVVSVLTVLH 240

Qy      313 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK 372
            |||||||||||||||||||||||||| ||||||||||||||:|:||||||||||||
Db      241 QDWLNGKEYKCKVSNKALPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVK 300

Qy      373 GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE 432
            |||||||||||||:||||||| ||||||||||||||||:|||||||||:||||||||||
Db      301 GFYPSDIAVEWESSGQPENNYNTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHE 360

Qy      433 ALHNHYTQKSLSLSPGK 449
            |||| :||||||||||
Db      361 ALHNRFTQKSLSLSPGK 377
```

RESULT 4
G2HU
Ig gamma-2 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 09-Jul-2004
C;Accession: A93906; A92809; A90752; A93132; A02148
R;Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
A;Reference number: A93906; MUID:82197621; PMID:6804948
A;Accession: A93906
A;Molecule type: DNA
A;Residues: 1-326 <ELL>
A;Cross-references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; P
A;Note: Lys-326 is probably removed posttranslationally
R;Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
A;Reference number: A92809; MUID:81007873; PMID:6774012
A;Contents: myeloma protein Til
A;Accession: A92809
A;Molecule type: protein
A;Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <WAN>
A;Note: Trp-156 is at or near the complement-binding site
R;Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A;Title: The amino acid sequences of the three heavy chain constant region domains of a
A;Reference number: A90752; MUID:80001357; PMID:113060
A;Contents: myeloma protein Zie
A;Accession: A90752
A;Molecule type: protein
A;Residues: 1-24,'E',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198-
A;Note: this sequence has since been revised
R;Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
A;Reference number: A93132; MUID:80114419; PMID:118920
A;Contents: Zie
A;Accession: A93132
A;Molecule type: protein
A;Residues: 238-275 <HOF>
R;Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A;Reference number: A94591
A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidat
ned
R;Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A;Reference number: A90253; MUID:72033500; PMID:4940472
A;Contents: annotation; myeloma protein Sa, disulfide bonds
R;Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A;Title: Structural studies of immunoglobulin G.
A;Reference number: A93157; MUID:69064124; PMID:5782707
A;Contents: annotation; Sa, disulfide bonds
C;Genetics:
A;Gene: GDB:IGHG2
A;Cross-references: GDB:119338; OMIM:147110
A;Map position: 14q32.33-14q32.33
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka;
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into l
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;133-202/Domain: immunoglobulin homology <IM2>
F;239-306/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83,140-200,246-304/Disulfide bonds: #status experimental
F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 52.2%; Score 1604; DB 1; Length 326;
Best Local Similarity 91.2%; Pred. No. 7.7e-83;
Matches 301; Conservative 12; Mismatches 13; Indels 4; Gaps 2;

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Qy      120 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
            |||||||||||||| |:|||  ||||||||||||||||||||||||||||||||||||||
Db        1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy      180 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 239
            |||||||||||||: ||||| |||:|||||||||| || | | :   |||||| : |
Db       61 GLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVE---CPPCPAPP-VAG 116

Qy      240 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299
            ||||||||||||||||||||||||||||||||||:|||||||||||||||||:|
Db      117 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFN 176

Qy      300 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359
            ||:||||||||:|||||||||||||| |||||||||| ||||||||||||||||:|
Db      177 STFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREE 236

Qy      360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSPFLYSKLTVDKSRW 419
            :|||||||||||||||||||||||||||||||||||:|||||||||||||||||||
Db      237 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRW 296

Qy      420 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
            ||||||||||||||||||||||||||||||
Db      297 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 326
```

RESULT 5
G4HU
Ig gamma-4 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
C;Accession: A90933; A90249; A02150
R;Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

```
A;Reference number: A90933; MUID:83157104; PMID:6299662
A;Accession: A90933
A;Molecule type: DNA
A;Residues: 1-327 <ELL>
A;Cross-references: UNIPROT:P01861
A;Note: the sequence was determined from the germline gene
R;Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A;Title: Human immunoglobulin sublclasses. Partial amino acid sequence of the constant r
A;Reference number: A90249; MUID:70207560; PMID:4192699
A;Accession: A90249
A;Molecule type: protein
A;Residues: 1-30;81-326 <PIN>
C;Genetics:
A;Gene: GDB:IGHG4
A;Cross-references: GDB:119340; OMIM:147130
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 111/1; 221/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;99-110/Region: hinge
F;134-203/Domain: immunoglobulin homology <IM2>
F;240-307/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83,141-201,247-305/Disulfide bonds: #status predicted
F;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;177/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             51.8%;  Score 1590.5;  DB 1;  Length 327;
  Best Local Similarity   90.9%;  Pred. No. 4.4e-82;
  Matches  300;  Conservative   12;  Mismatches   15;  Indels    3;  Gaps    1;

Qy        120 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
              ||||||||||||| |:||| ||||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy        180 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 239
              |||||||||||||||||:|| |||:||||||||||:|| |       || ||||| |||
Db         61 GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESK---YGPPCPSCPAPEFLGG 117

Qy        240 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299
              |||||||||||||||||||||||||||||| |||||:||||||||||||||||||||:|
Db        118 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFN 177

Qy        300 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359
              |||||||||||||||||||||||||||||| ||: ||||||||||||||||||||::|
Db        178 STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEE 237

Qy        360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 419
              :||||||||||||||||||||||||||||||||||||||||||||||||:||||||||
Db        238 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRW 297

Qy        420 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |:||||||||||||||||||||||| ||
Db        298 QEGNVFSCSVMHEALHNHYTQKSLSLSLGK 327


RESULT 6
PC4436
monoclonal antibody 13-1 heavy chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C;Accession: PC4436
R;Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.
Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A;Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyr
A;Reference number: JC5810; MUID:98063277; PMID:9398605
A;Accession: PC4436
A;Molecule type: protein
A;Residues: 1-444 <AKA>
C;Comment: This catalytic antibody has peroxidase oxidase activity. It is directed again
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;251-320/Domain: immunoglobulin homology <IMM>
F;22/Disulfide bonds: interchain (to 98) #status predicted
F;99/Disulfide bonds: interchain (to 109) #status predicted

  Query Match             49.1%;  Score 1508.5;  DB 2;  Length 444;
  Best Local Similarity   61.1%;  Pred. No. 2.5e-77;
  Matches  277;  Conservative   73;  Mismatches   90;  Indels   13;  Gaps    6;

Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYIS--SGGSGT 58
              ||| ||:||  |:|| ||::||  ||| ||:| | |:|| ||| |||:| |:  |   |
Db          1 EVQXVETGGGLVRPGNSLKLSCLTSGFTFSNYRMHWLRQPPGKRLEWIAVITVKSDNYGA 60

Qy         59 YYSDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYFDSWGQGTLLTVS 118
               |::||:||||||||:||:::||||  || ||:| |:| |     |  | ||||| : ||
Db         61 KYAESVRGRFTISRDDSKSSVYLQMNRLREEDTATYYCCRTP-WVYAMDCWGQGTSVIVS 119

Qy        119 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 178
              || |  |||:|||| | : :     |||||| |||||||:||||:|:||||||||||||
Db        120 SAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQS 179

Qy        179 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP--CPAPEL 236
               ||:||| ||||||:  ::|  ||| |  |:|||||: |: |     | |  |  ||:
Db        180 D-LYTLSSSVTVPSSTWPSETVTCNVAHPASSTKVDKKIVPRDCG----CKPCICTVPEV 234

Qy        237 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 296
                |||:||||||| | |: ||:|||||||:| :||||:|:|:|| |||| |:|:||||
Db        235 ---SSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREE 291

Qy        297 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 356
              |:|||:| || | ::|||||||||:||:|:: | |||||||||| ||:|: |||||:||
Db        292 QFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPP 351

Qy        357 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 416
              :::: |::|||||::  |:| || ||||: ||||  ||| | |::|:|||:|:|||| | |
Db        352 KEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNVQK 411

Qy        417 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              | |: || |:|||:|| ||||:|:|||| ||||
Db        412 SNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK 444


RESULT 7
S22080
Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine
N;Alternate names: Ig gamma-1 chain C region (clone 8.10)
C;Species: Bos primigenius taurus (cattle)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S22080; S06610; A31303
R;Sanders, P.G.
submitted to the EMBL Data Library, November 1991
A;Reference number: S22080
A;Accession: S22080
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-470 <SAN>
A;Cross-references: EMBL:X62916; NID:g439; PIDN:CAA44699.1; PID:g440
R;Symons, D.B.A.; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989
A;Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamm
A;Reference number: S06610; MUID:90097956; PMID:2513487
A;Accession: S06610
A;Molecule type: DNA
A;Residues: 142-470 <SYM>
A;Cross-references: EMBL:X16701
A;Note: the sequence was determined from the germline gene
C;Genetics:
A;Gene: Ig CH gamma-1
A;Introns: 98/1; 111/1; 221/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein
F;161-225/Domain: immunoglobulin homology <IMM>
```

```
F;318/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match            48.4%;  Score 1487;  DB 2;  Length 470;
  Best Local Similarity  62.4%;  Pred. No. 4.3e-76;
  Matches  284;  Conservative   60;  Mismatches  101;  Indels   10;  Gaps    6;

Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60
              :||| |||   |:|  :| ::|  |||: | ||::|||||||| ||||  |:|||: |||
Db         20 QVQLRESGPSLVKPSQTLSLTCTVSGFSLSSYALTWVRQAPGKALEWVGGITSGGT-TYY 78

Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTY----YFDSWGQGTLLT 116
              : ::| | :|:::|||: : | : |:  ||:| |:| |   |        |:|||| |:|
Db         79 NPALKSRLSITKENSKSQVSLSVSSVTPEDTATYYCARSTYGEVGDGAIADAWGQGLLVT 138

Qy        117 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 176
              ||||||  | |:||:      |  |  |||||  | ||||||:|||||| ||||||||||
Db        139 VSSASTTAPKVYPLSSCCGDKSSSTVTLGCLVSSYMPEPVTVTWNSGALKSGVHTFPAVL 198

Qy        177 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 236
              |||||||||:|||| |: | ||: ||| |  |:|||| |:| :| |   |  || |||
Db        199 QSSGLYSLSSMVTVPGSTSG-QTFTCNVAHPASSTKVDKAVDP-TC-KPSPCDCCPPPEL 255

Qy        237 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 296
              ||||||:|||||||| || |||||||||| |:||||||:|:|| |||: | ||||||
Db        256 PGGPSVFIFPPKPKDTLTISGTPEVTCVVVDVGHDDPEVKFSWFVDDVEVNTATTKPREE 315

Qy        297 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 356
              |:|||||||| | : ||||  |||:|||| |: ||||| :|||: ||  ||||||  | |
Db        316 QFNSTYRVVSALRIQHQDWTGGKEFKCKVHNEGLPAPIVRTISRTKGPAREPQVYVLAPP 375

Qy        357 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGSFFLYSKLTV 414
              ::||:|: |||||:|  |||  |||||: ||||  |: | |||| ||:|  |:|||||  |
Db        376 QEELSKSTVSLTCMVTSFYPDYIAVEWQRNGQPESEDKYGTTPPQLDADSSYFLYSKLRV 435

Qy        415 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |:: ||:|: ::| |||||||||||||| | | ||
Db        436 DRNSWQEGDTYTCVVMHEALHNHYTQKSTSKSAGK 470


RESULT 8
S37483
Ig gamma-2a chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37483
R;Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A;Reference number: S37483
A;Accession: S37483
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-469 <DUC>
A;Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;276-345/Domain: immunoglobulin homology <IMM>

  Query Match            46.9%;  Score 1440.5;  DB 2;  Length 469;
  Best Local Similarity  59.1%;  Pred. No. 1.7e-73;
  Matches  267;  Conservative   72;  Mismatches  108;  Indels    5;  Gaps    4;

Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60
              ::|| :|| : |:|| |:::|| |||: |: | ::||:| ||:||:|: :|      | |
Db         20 QIQLQQSGPELVKPGASVKISCKASGYTFTDYYINWVKQKPGQGLKWIGWIYPASGNTKY 79

Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGT-YYFDSWGQGTLLTVSS 119
              ::: ||: |:: | | :|:|:|: || :||:|||||| |     |     | ||||| |||||
Db         80 NENFKGKATLTVDTSSSTAYMQLSSLTSEDTAVYFCARAMGATATLLDYWGQGTTLTVSS 139

Qy        120 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
              | |  |||:||||    |:| :  |||||| |||||||::||||:|:||||||||||||
Db        140 AKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSD 199

Qy        180 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP--CPAPELL 237
              ||:||| ||| ||:  :|:  ||| |  |:||||||:||:       |||  |||| ||
Db        200 -LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRG-PTIKPCPPCKCPAPNLL 257

Qy        238 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297
              ||||||:|||| || |||| :| |||||||| :||:|: :|:|: |||| |:|:   |
Db        258 GGPSVFIFPPKIKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHRED 317

Qy        298 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 357
              |||| |||| | : ||||::|||:||||:|| ||||||:|||| ||  | |||| |||
Db        318 YNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPPE 377

Qy        358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 417
              :|:|| ||:|||:|  | | || ||| :||: | ||| | |||||||:|:|||| |:|
Db        378 EEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKK 437

Qy        418 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              | : | :||||:|| ||||:| || | :|||
Db        438 NWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK 469


RESULT 9
S40295
Ig gamma-2a chain (mAb735) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C;Accession: S40295
R;Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; B
submitted to the EMBL Data Library, January 1993
A;Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against
A;Reference number: S40295
A;Accession: S40295
A;Molecule type: protein
A;Residues: 1-446 <KLE>
A;Cross-references: UNIPROT:Q99L25
C;Genetics:
A;Map position: 12
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid
F;1-446/Product: Ig gamma-2a chain #status experimental <MAT>
F;1-117/Domain: V-D-J region <VDJ>
F;118-446/Domain: C region <CHR>
F;118-214/Domain: C1 region <CH1>
F;215-230/Region: hinge
F;231-340/Domain: C2 region <CH2>
F;341-446/Domain: C3 region <CH3>
F;360-427/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted
F;132/Disulfide bonds: interchain (to light chain) #status predicted
F;224,227,229/Disulfide bonds: interchain #status predicted
F;297/Binding site: carbohydrate (Asn) (covalent) #status experimental

  Query Match            46.8%;  Score 1437;  DB 2;  Length 446;
  Best Local Similarity  59.3%;  Pred. No. 2.5e-73;
  Matches  267;  Conservative   70;  Mismatches  107;  Indels    6;  Gaps    4;

Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60
              ::|| :|| : |:|| |:::|| |||: |: | : ||:| ||:||||: :|   |   | |
Db          1 QIQLQQSGPELVRPGASVKISCKASGYTFTDYYIHWVKQRPGEGLEWIGWIYPGSGNTKY 60

Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYFDSWGQGTLLTVSSA 120
              ::  ||: |:: | | :| |:|: || :||||||| |   | : | ||||| :|||||
Db         61 NEKFKGKATLTVDTSSSTAYMQLSSLTSEDSAVYFCARG--GKFAMDYWGQGTSVTVSSA 118

Qy        121 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180
              |  |||:||||    |:| :  |||||| |||||||::||||:|:||||||||||||
Db        119 KTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSD- 177

Qy        181 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP--CPAPELLG 238
              ||:||| ||| ||:  :|:  ||| |  |:||||||:||:       |||  |||| |||
Db        178 LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRG-PTIKPCPPCKCPAPNLLG 236
```

```
Qy        239 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 298
              |||||:|||| || |||| :| ||||||||| :||:|: :|:|: |||  |:|:   | |
Db        237 GPSVFIFPPKIKDVLMISLSPMVTCVVVDVSEDDPDVQISWFVNNVEVLTAQTQTHREDY 296

Qy        299 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 358
              ||| |||| | : ||||::|||:||||:|| ||||||:|||| ||  | |||| |||  :
Db        297 NSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPPEE 356

Qy        359 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 418
              |:|| ||:|||:|  | | || ||| :||: | ||| | ||||||||:|:|||| |:|
Db        357 EMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKN 416

Qy        419 WQQGNVFSCSVMHEALHNHYTQKSLSLSPG 448
              | : | :||||:|| ||||:| || | :||
Db        417 WVERNSYSCSVVHEGLHNHHTTKSFSRTPG 446


RESULT 10
S31459
Ig gamma-1 chain - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C;Accession: S31459
R;Patri, S.; Nau, F.
submitted to the EMBL Data Library, December 1992
A;Reference number: S31459
A;Accession: S31459
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-472 <PAT>
A;Cross-references: EMBL:X69797
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;277-346/Domain: immunoglobulin homology <IMM>

  Query Match             46.7%;  Score 1434;  DB 2;  Length 472;
  Best Local Similarity   59.4%;  Pred. No. 4e-73;
  Matches  274;  Conservative   64;  Mismatches  105;  Indels   18;  Gaps    5;

Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSG--- 57
              :|:| |||        :| |:|  |||: ::| : |||||||| |||:     ||||
Db         18 QVRLQESGPSLATLLQTLSVTCTISGFSLNNYGVDWVRQAPGKALEWL-----GGSGYDE 72

Qy         58 -TYYSDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTYY------FDSWG 110
               |:  :| | :|::| ||: : | : ::  ||:|||:| ||   : :      :| ||
Db         73 DIDYNPVLKSRLSITKDTSKSQVSLTLSTVTTEDTAVYYCARVDYDSSHAFAYASYDFWG 132

Qy        111 QGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 170
              | |::| |||| | |:||      ||     |||||  | ||||||:||||||||||
Db        133 PGLLISVLSASTTPPKVYPLTSCCGDTSSSIVTLGCLVSSYMPEPVTVTWNSGALTSGVH 192

Qy        171 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP 230
              ||||:|||||||||||||||:|: | ||:|||| |  |:|||||:|||   |    |
Db        193 TFPAILQSSGLYSLSSVVTVPASTSGAQTFICNVAHPASSTKVDKRVEPGCPDPCKHC-R 251

Qy        231 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 290
              || ||| ||||||:|||||||||| || |||||||||||  :||||:|:|:|| |||  |:
Db        252 CPPPELPGGPSVFIFPPKPKDTLTISGTPEVTCVVVDVGQDDPEVQFSWFVDNVEVRTAR 311

Qy        291 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 350
              |||||||:|||:|||| | : ||||  |||:|||| |:|||||| :|||: ||| |||||
Db        312 TKPREEQFNSTFRVVSALPIQHQDWTGGKEFKCKVHNEALPAPIVRTISRTKGQAREPQV 371

Qy        351 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGSFFL 408
              | | | ::||:|: :|:|||| ||||  |||||: ||||  |: | ||   ||:|||:||
Db        372 YVLAPPQEELSKSTLSVTCLVTGFYPDYIAVEWQKNGQPESEDKYGTTTSQLDADGSYFL 431

Qy        409 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              ||:| |||: ||:|: ::| |||||||||||||:|  |||
Db        432 YSRLRVDKNSWQEGDTYACVVMHEALHNHYTQKSISKPPGK 472


RESULT 11
S69339
Ig heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C;Accession: S69339; S72664
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A;Reference number: S69339; MUID:95262687; PMID:7744049
A;Accession: S69339
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <KHA>
A;Cross-references: EMBL:X81695
R;Khamlichi, A.A.
submitted to the EMBL Data Library, September 1994
A;Reference number: S72664
A;Accession: S72664
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140,'C',142-374 <KH2>
A;Cross-references: EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology

  Query Match             46.5%;  Score 1429;  DB 2;  Length 374;
  Best Local Similarity   62.1%;  Pred. No. 5.7e-73;
  Matches  282;  Conservative   23;  Mismatches   45;  Indels  104;  Gaps    4;

Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSH--YAMSWVRQAPGKGLEWVAYISSGGSGT 58
              :: | |||   |:|  :| ::|  |||: |     : |:|| ||: |||:| |
Db         20 QITLKESGPTLVKPTQTLTLTCTFSGFSLSKSGVGVGWIRQPPGQALEWLALI-FWDDDK 78

Qy         59 YYSDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLG---TYYFDSWGQGTLL 115
               || |:: | ||::| ||| : | | ::   |:| |:|     |    | | |||||||:
Db         79 RYSPSLRTRLTITKDTSKNQVVLTMTNVDPADTATYYCGYSVEGYGQGYRFHSWGQGTLV 138

Qy        116 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 175
              ||||
Db        139 TVSS---------------------------------------------------------- 142

Qy        176 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE 235
                                                   ||||||||||||||||||
Db        143 ------------------------------------------EPKSCDKTHTCPPCPAPE 160

Qy        236 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 220

Qy        296 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 280

Qy        356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 415
              ||:|:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 340

Qy        416 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              ||||||||||||||||||||||||||||||||||
Db        341 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 374


RESULT 12
G2MS11
Ig gamma-2b chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1980 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: S25057; A02157; A26235; A26232; A26233; A53598
R;Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
submitted to the EMBL Data Library, July 1992
A;Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific m
A;Reference number: S25057
A;Accession: S25057
A;Status: preliminary
```

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A;Molecule type: mRNA
A;Residues: 1-474 <PIS>
A;Cross-references: UNIPROT:P01866; EMBL:X67210; NID:g54826; PIDN:CAA47649.1; PID:g54827
R;Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
Nature 283, 786-789, 1980
A;Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from r
A;Reference number: A02157; MUID:80120716; PMID:6766534
A;Contents: a allele
A;Accession: A02157
A;Molecule type: DNA
A;Residues: 138-161,'L',163-189,'FP',193-474 <YAM>
A;Cross-references: GB:J00461
A;Note: the sequence was determined from the germline gene
R;Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.
Science 206, 1299-1303, 1979
A;Title: Structure of the constant and 3' untranslated regions of the murine gamma2b hea
A;Reference number: A26235; MUID:80081501; PMID:117548
A;Contents: MPC 11
A;Accession: A26235
A;Molecule type: mRNA
A;Residues: 138-172,'P',174-189,'FP',193-376,'T',378-474 <TU1>
A;Note: Lys-474 is probably removed posttranslationally
R;Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.
Science 206, 1303-1306, 1979
A;Title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglo
A;Reference number: A26232; MUID:80081502; PMID:117549
A;Accession: A26232
A;Molecule type: DNA
A;Residues: 138-172,'P',174-189,'FP',193-376,'T',378-474 <TU2>
R;Ollo, R.; Rougeon, F.
Nature 296, 761-763, 1982
A;Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamm
A;Reference number: A26233; MUID:82173203; PMID:6803173
A;Contents: b allele
A;Accession: A26233
A;Molecule type: DNA
A;Residues: 138-161,'L',163-189,'FP',193-300,'R',302-331,'A',333-437,'DI',440-474 <OLL>
A;Cross-references: GB:J00461
R;Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahash
J. Biol. Chem. 269, 12345-12350, 1994
A;Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.
A;Reference number: A53598; MUID:94216359; PMID:7512967
A;Accession: A53598
A;Status: preliminary
A;Molecule type: protein
A;Residues: 234-251 <KIM>
C;Comment: The a allele sequence is shown.
C;Genetics:
A;Introns: 138/1; 236/1; 258/1; 368/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobu
F;157-222/Domain: immunoglobulin homology <IM1>
F;236-257/Region: hinge
F;281-350/Domain: immunoglobulin homology <IM2>
F;387-454/Domain: immunoglobulin homology <IM3>
F;152/Disulfide bonds: interchain (to light chain) #status predicted
F;164-220,288-348,394-452/Disulfide bonds: #status predicted
F;247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicted
F;324/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             45.3%;  Score 1390;  DB 1;  Length 474;
  Best Local Similarity   56.6%;  Pred. No. 1.2e-70;
  Matches  260;  Conservative   72;  Mismatches  113;  Indels   14;  Gaps    4;

Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60
              |||| :|| : | || |:::|| |||: |  | | ||:| ||:||||: ||:    || :
Db         20 EVQLQQSGPELVNPGASVKMSCKASGYTFITYVMHWVKQKPGQGLEWIGYINPNKDGTKF 79

Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTY---YFDSWGQGTLLTV 117
              ::  ||: |:: | | || |::: || :||||||:| |     |   :|  ||||||:||
Db         80 NEKFKGKATLTSDKSSNTAYMELSSLTSEDSAVYYCAR----DYDYDWFAYWGQGTLVTV 135

Qy        118 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 177
              |:| |  |||:||||    |:| :   ||||| |||| |||:||||:|:| |||    |
Db        136 SAAKTTPPSVYPLAPGCGDTTGSSVTSGCLVKGYFPESVTVTWNSGSLSSSVHTLSQALL 195

Qy        178 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT-HTCPP------ 230
              ||||::|| ||||||:  :||  |:| |  |:| ||||:||     | : |||
Db        196 QSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECHK 255

Qy        231 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 290
              |||| | ||||||:|||  || |||| ||:|||||||| :||:|: :|:|: |||| |:
Db        256 CPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQ 315

Qy        291 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 350
              |:  | |||| |||| | : ||||::|||:||||:|| ||:|||:|||| ||  | |||
Db        316 TQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQV 375

Qy        351 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 410
              | |||  ::|::  ||||||| || | ||:||| |||  | ||| | ||||||||:|:||
Db        376 YILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYS 435

Qy        411 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              || :  |:|:: : |||:| || | |:| :|::| ||||
Db        436 KLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 474


RESULT 13
S01321
Ig gamma-2b chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
C;Accession: S01321
R;de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
Eur. J. Biochem. 176, 287-295, 1988
A;Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed
A;Reference number: S01320; MUID:88329081; PMID:3138116
A;Accession: S01321
A;Molecule type: mRNA
A;Residues: 1-475 <DE1>
A;Cross-references: EMBL:X13188; NID:g51780; PIDN:CAA31580.1; PID:g51781
A;Note: this sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-475/Product: Ig gamma-2b chain #status predicted <MAT>
F;159-223/Domain: immunoglobulin homology <IMM>

  Query Match             44.5%;  Score 1367.5;  DB 2;  Length 475;
  Best Local Similarity   56.2%;  Pred. No. 2.1e-69;
  Matches  257;  Conservative   75;  Mismatches  116;  Indels    9;  Gaps    4;

Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60
              :||| :|| :  :|| |:::|| |||:  : | :|||:|  |:||||:  |  |   :|:
Db         20 QVQLQQSGAELARPGASVKLSCKASGYTLTSYGISWVKQRTGQGLEWIGEIYPGSGNSYF 79

Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVK-LGTYYFDSWGQGTLLTVSS 119
              ::  ||: |:: | | :| || : || :|||||||   : :|   |  ||||||:| |:
Db         80 NEKFKGKATLTVDKSSSTAYLHLSSLTSEDSAVYFCAGPRQVGLLPFGYWGQGTLVTASA 139

Qy        120 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
              | |  |||:||||    |:| :  |||||| |||| |||:||||:|:| ||||||:|| |
Db        140 AKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQ-S 198

Qy        180 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT-HTCPP------CP 232
              |||::|| ||||||:  :||  |:| |  |:| ||||:||     | : |||      ||
Db        199 GLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPTSTINPCPPCKECHKCP 258

Qy        233 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 292
              || | ||||||:|||  || |||| ||:|||||||| :||:|: :|:|: |||  |:|:
Db        259 APNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVLTAQTQ 318

Qy        293 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT 352
                | |||| |||| | : ||||::|||:||||:|| ||||||:|||| ||  | ||||
```

```
Db        319 THREDYNSTIRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKIKGIVRAPQVYI 378

Qy        353 LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL 412
              | |  ::|::  |||||  || | ||:||| |||  | ||| | |||||||:|:||||
Db        379 LSPPPEQLSRKDVSLTCLAVGFSPEDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKL 438

Qy        413 TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
               :  |:|:: : |||:| || | |:| :|::| ||||
Db        439 NMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 475


RESULT 14
I47159
Ig gamma 2a chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47159
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47159
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124
C;Genetics:
A;Gene: IgG2a
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>

  Query Match             41.1%;  Score 1263;  DB 2;  Length 328;
  Best Local Similarity   69.6%;  Pred. No. 9.4e-64;
  Matches  231;  Conservative   43;  Mismatches   52;  Indels    6;  Gaps    2;

Qy        120 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
              |   |||:|||| |: |||   |||||   ||||||||:||||||:|||||||:||| |
Db          1 APKTAPSVYPLAPCSRDTSGPNVALGCLASSYFPEPVTVTWNSGALSSGVHTFPSVLQPS 60

Qy        180 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 239
              |||||||:||||:||| :::| |||||  : |||||:|  |:      || | :|    |
Db         61 GLYSLSSMVTVPASSLSSKSYTCNVNHPATTTKVDKRVGTKTKPPCPICPACESP----G 116

Qy        240 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299
              ||||:|||||||||||||:||||||||| |:|||:|:|||||||| |:|:|:|:||:|
Db        117 PSVFIFPPKPKDTLMISRTPQVTCVVVDVSQENPEVQFSWYVDGVEVHTAQTRPKEEQFN 176

Qy        300 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359
              ||||||||| : |||||||||:||||:|| ||||| : ||||||| ||||||||||  :|
Db        177 STYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAKGQTREPQVYTLPPHAEE 236

Qy        360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGSFFLYSKLTVDKS 417
              |::::||:|||| |||| || |||: |||  || ||:||||  | ||::||||| :|||:
Db        237 LSRSKVSITCLVIGFYPPDIDVEWQRNGQPEPEGNYRTTPPQQDVDGTYFLYSKFSVDKA 296

Qy        418 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
               || | :| |:||||||||||||||:| :|||
Db        297 SWQGGGIFQCAVMHEALHNHYTQKSISKTPGK 328


RESULT 15
S31866
Ig gamma-1 chain C region - synthetic
C;Species: synthetic
A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C;Accession: S31866
R;Pilpula, D.
submitted to the EMBL Data Library, February 1993
A;Description: Screeing method for protein-protein interactions of cloned gene products.
A;Reference number: S31866
A;Accession: S31866
A;Molecule type: mRNA
A;Residues: 1-255 <FIL>
A;Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
C;Keywords: immunoglobulin
F;1-22/Region: Escherichia coli outer membrane protein A precursor
F;23-255/Region: human Ig gamma-1 chain C region

  Query Match             41.0%;  Score 1260;  DB 4;  Length 255;
  Best Local Similarity   97.5%;  Pred. No. 1e-63;
  Matches  233;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy        211 TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH 270
              |     || ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 TVAQADVESKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH 76

Qy        271 EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL 330
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL 136

Qy        331 PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE 390
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE 196

Qy        391 NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 255


Search completed: December 23, 2004, 19:06:04
Job time : 33.449 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2004, 18:31:20 ; Search time 161.904 Seconds
(without alignments)
2068.313 Million cell updates/sec

Title: US-10-089-500-53
Perfect score: 3071
Sequence: 1 EVQLVESGGDFVQPGGSLRV.....IVEFLNRWITFCQSIISTLT 582

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2226.5	72.5	471	2	AAH24289	Aah24289 homo sapi
2	2223	72.4	470	2	Q6PJA4	Q6pja4 homo sapien
3	2223	72.4	470	2	AAH18747	Aah18747 homo sapi
4	2212	72.0	478	2	Q6PI81	Q6pi81 homo sapien
5	2212	72.0	478	2	AAH41037	Aah41037 homo sapi
6	2211.5	72.0	475	2	Q6MZQ6	Q6mzq6 homo sapien
7	2211.5	72.0	475	2	CAE45972	Cae45972 homo sapi
8	2191.5	71.4	473	2	Q6MZV7	Q6mzv7 homo sapien
9	2191.5	71.4	473	2	CAE45920	Cae45920 homo sapi
10	2191	71.3	472	2	BAC85232	Bac85232 homo sapi
11	2188.5	71.3	475	2	Q6GMW7	Q6gmw7 homo sapien
12	2187	71.2	466	2	Q6IN78	Q6in78 homo sapien
13	2187	71.2	472	2	Q6N089	Q6n089 homo sapien
14	2187	71.2	472	2	CAE45781	Cae45781 homo sapi
15	2185.5	71.2	479	2	AAH06402	Aah06402 homo sapi
16	2184.5	71.1	544	2	Q6PJ95	Q6pj95 homo sapien
17	2184.5	71.1	544	2	AAH19046	Aah19046 homo sapi
18	2173	70.8	468	2	BAC85444	Bac85444 homo sapi
19	2172	70.7	480	2	Q6N094	Q6n094 homo sapien
20	2172	70.7	480	2	CAE45776	Cae45776 homo sapi
21	2159	70.3	466	2	Q6N096	Q6n096 homo sapien
22	2159	70.3	466	2	CAE45774	Cae45774 homo sapi
23	2158	70.3	470	2	Q7Z5W1	Q7z5w1 homo sapien
24	2149.5	70.0	473	2	Q6P055	Q6p055 homo sapien
25	2149.5	70.0	473	2	AAH65820	Aah65820 homo sapi
26	2147.5	69.9	471	2	BAC85388	Bac85388 homo sapi
27	2145	69.8	470	2	BAC85172	Bac85172 homo sapi
28	2144	69.8	466	2	AAH64496	Aah64496 homo sapi
29	2142	69.7	478	2	BAC85385	Bac85385 homo sapi
30	2136	69.6	464	2	BAC85373	Bac85373 homo sapi
31	2134	69.5	482	2	Q7Z351	Q7z351 homo sapien
32	2123	69.1	474	2	BAC85350	Bac85350 homo sapi
33	2113.5	68.8	479	2	AAH14667	Aah14667 homo sapi
34	2109	68.7	464	2	AAH19337	Aah19337 homo sapi
35	2107	68.6	468	2	BAC85175	Bac85175 homo sapi
36	2105.5	68.6	481	2	Q6N097	Q6n097 homo sapien
37	2105.5	68.6	481	2	CAE45773	Cae45773 homo sapi
38	2096	68.3	474	2	BAC85171	Bac85171 homo sapi
39	2084	67.9	472	2	BAC86225	Bac86225 homo sapi
40	2083.5	67.8	469	2	Q7Z7P5	Q7z7p5 homo sapien
41	2082	67.8	470	2	AAH62336	Aah62336 homo sapi
42	2076	67.6	476	2	BAC05017	Bac05017 homo sapi
43	2075	67.6	478	2	BAC86514	Bac86514 homo sapi
44	2070	67.4	474	2	BAC05012	Bac05012 homo sapi
45	2069.5	67.4	473	2	BAC05013	Bac05013 homo sapi

ALIGNMENTS

RESULT 1
AAH24289
ID AAH24289 PRELIMINARY; PRT; 471 AA.
AC AAH24289;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC024289; AAH24289.1; -.
KW Hypothetical protein.
SQ SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;

Query Match 72.5%; Score 2226.5; DB 2; Length 471;
Best Local Similarity 92.9%; Pred. No. 7.7e-137;
Matches 420; Conservative 15; Mismatches 14; Indels 3; Gaps 2;

```
Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60
              |||||||||  |:||||||:||||||| || |:|:|||||||||||||: :||  |  ||
Db         20 EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSMSSSSSYIYY 79

Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTR--VKLGTY-YFDSWGQGTLLTV 117
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           :|||||||||||||:||:|||||  ||||||:|||:| |   :| :| ||| ||:|||:||
Db         80 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDLRQLTSYWYFDLWGRGTLVTV 139

Qy        118 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 199

Qy        178 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 259

Qy        238 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 319

Qy        298 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 379

Qy        358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 439

Qy        418 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              ||||||||||||||||||||||||||||||||
Db        440 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 471


RESULT 2
Q6PJA4
ID   Q6PJA4      PRELIMINARY;      PRT;   470 AA.
AC   Q6PJA4;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC018747; AAH18747.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   470 AA;  51715 MW;  7B49556A11FD7D99 CRC64;

  Query Match            72.4%;  Score 2223;  DB 2;  Length 470;
  Best Local Similarity  93.1%;  Pred. No. 1.3e-136;
  Matches  420;  Conservative    7;  Mismatches   22;  Indels    2;  Gaps    1;

Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60
              |||||||||  ||||||||:||  ||| || | |||||||||||||||||  |    ||  ||
Db         20 EVQLVESGGGLVQPGGSLRLSCVVSGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYY 79

Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTY--YFDSWGQGTLLTVS 118
               |||||||||||||:||:||||| ||||||:|||:| |      |  :|| ||||||:|||
Db         80 VDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDGSSWYRDWFDPWGQGTLVTVS 139

Qy        119 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 199

Qy        179 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 259

Qy        239 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 319

Qy        299 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 379

Qy        359 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 418
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 439

Qy        419 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              ||||||||||||||||||||||||||||||
Db        440 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470


RESULT 3
AAH18747
ID   AAH18747    PRELIMINARY;      PRT;   470 AA.
AC   AAH18747;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
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RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC018747; AAH18747.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   470 AA;  51715 MW;  7B49556A11FD7D99 CRC64;

  Query Match            72.4%;  Score 2223;  DB 2;  Length 470;
  Best Local Similarity  93.1%;  Pred. No. 1.3e-136;
  Matches  420;  Conservative    7;  Mismatches   22;  Indels    2;  Gaps    1;

Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60
              |||||||||  ||||||||:||   ||| || | |||||||||||||||| |    ||  ||
Db         20 EVQLVESGGGLVQPGGSLRLSCVVSGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYY 79

Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTY--YFDSWGQGTLLTVS 118
                |||||||||||||:||:||||| ||||||:|||:| |      |  :|| ||||||:|||
Db         80 VDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDGSSWYRDWFDPWGQGTLVTVS 139

Qy        119 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 199

Qy        179 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 259

Qy        239 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 319

Qy        299 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 379

Qy        359 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 418
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 439

Qy        419 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||||||||||||||||
Db        440 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470


RESULT 4
Q6PI81
ID   Q6PI81      PRELIMINARY;      PRT;   478 AA.
AC   Q6PI81;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC041037; AAH41037.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   478 AA;  52666 MW;  17BED38D917970D6 CRC64;

  Query Match            72.0%;  Score 2212;  DB 2;  Length 478;
  Best Local Similarity  91.3%;  Pred. No. 6.9e-136;
  Matches  419;  Conservative   10;  Mismatches   20;  Indels   10;  Gaps    2;

Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60
              |||||||||  ||||||||:|||||| || | |||||||||||||||| |    ||  ||
Db         20 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYY 79

Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTR--------VKLGTYYF--DSWG 110
                |||||||||||||:||:||||| ||||||:|||:| |        |    |||  | ||
Db         80 VDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREFESTMTTVNADYYYFYMDVWG 139

Qy        111 QGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 170
              :|| :||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 KGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 199

Qy        171 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP 230
              ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||
Db        200 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPP 259

Qy        231 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 319

Qy        291 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 350
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 379

Qy        351 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 410
              |||||||:|:||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 439
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Qy        411 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||||||||||||||||||||||||
Db        440 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
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RESULT 5
AAH41037
ID AAH41037 PRELIMINARY; PRT; 478 AA.
AC AAH41037;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC041037; AAH41037.1; -.
KW Hypothetical protein.
SQ SEQUENCE 478 AA; 52666 MW; 17BED38D917970D6 CRC64;

Query Match 72.0%; Score 2212; DB 2; Length 478;
Best Local Similarity 91.3%; Pred. No. 6.9e-136;
Matches 419; Conservative 10; Mismatches 20; Indels 10; Gaps 2;

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Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60
              |||||||||  ||||||||:|||||||  || | ||||||||||||||| |   ||  ||
Db         20 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYY 79

Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTR--------VKLGTYYF--DSWG 110
               |||||||||||||:||:|||||  ||||||:|||:| |        |    |||  | ||
Db         80 VDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREFESTMTTVNADYYYFYMDVWG 139

Qy        111 QGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 170
              :|| :|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 KGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 199

Qy        171 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP 230
              ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||
Db        200 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPP 259

Qy        231 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        260 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 319

Qy        291 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 350
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 379

Qy        351 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 410
              |||||||:|:||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 439

Qy        411 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||||||||||||||||||||||||
Db        440 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
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RESULT 6
Q6MZQ6
ID Q6MZQ6 PRELIMINARY; PRT; 475 AA.
AC Q6MZQ6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686G11190.
GN Name=DKFZp686G11190;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG THE GERMAN HUMAN CDNA CONSORTIUM;
RA Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BX640947; CAE45972.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF00047; ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8E CRC64;

Query Match 72.0%; Score 2211.5; DB 2; Length 475;
Best Local Similarity 91.2%; Pred. No. 7.4e-136;
Matches 416; Conservative 13; Mismatches 20; Indels 7; Gaps 1;

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Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60
              ||||:||||  ||||||||:||||||| | :|||:|||||||||||||: ||| |  |||
Db         20 EVQLLESGGGLVQPGGSLRLSCAASGFTFRNYAMNWVRQAPGKGLEWVSGISSSGVNTYY 79

Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTY-------YFDSWGQGT 113
              :||||||||||  | | ||||||| ||||:|:|||:| |     |       ||| ||:||
Db         80 ADSVKGRFTISGDISTNTLYLQMHSLRADDTAVYYCARADYRDYQVSPAYWYFDVWGRGT 139

Qy        114 LLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 173
              |::||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 LVSVSAASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 199

Qy        174 AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA 259

Qy        234 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        260 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 319

Qy        294 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 379

Qy        354 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 413
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 439

Qy        414 VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||| ||||||||||||||||
Db        440 VDKSRWQQGNVFSCSVMHEGLHNHYTQKSLSLSPGK 475


RESULT 7
CAE45972
ID   CAE45972    PRELIMINARY;      PRT;   475 AA.
AC   CAE45972;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein DKFZp686G11190.
GN   DKFZP686G11190.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Human esophagus tumor;
RA   Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA   Han M., Wiemann S.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX640947; CAE45972.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   475 AA;  52043 MW;  B7EAE255A26F4B8E CRC64;

  Query Match           72.0%;  Score 2211.5;  DB 2;  Length 475;
  Best Local Similarity  91.2%;  Pred. No. 7.4e-136;
  Matches  416;  Conservative   13;  Mismatches   20;  Indels    7;  Gaps    1;

Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60
              ||||:||||  |||||||:|||||| | :|||:|||||||||||||: ||| |  |||
Db         20 EVQLLESGGGLVQPGGSLRLSCAASGFTFRNYAMNWVRQAPGKGLEWVSGISSSGVNTYY 79

Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTY-------YFDSWGQGT 113
              :||||||||||  | | ||||||| ||||:|:|||:| |     |           ||| ||:||
Db         80 ADSVKGRFTISGDISTNTLYLQMHSLRADDTAVYYCARADYRDYQVSPAYWYFDVWGRGT 139

Qy        114 LLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 173
              |::||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 LVSVSAASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 199

Qy        174 AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA 259

Qy        234 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 319

Qy        294 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 379

Qy        354 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 413
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 439

Qy        414 VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||| ||||||||||||||||
Db        440 VDKSRWQQGNVFSCSVMHEGLHNHYTQKSLSLSPGK 475


RESULT 8
Q6MZV7
ID   Q6MZV7      PRELIMINARY;      PRT;   473 AA.
AC   Q6MZV7;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein DKFZp686C11235.
GN   Name=DKFZp686C11235;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Human small intestine;
RG   THE GERMAN HUMAN CDNA CONSORTIUM;
RA   Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX640853; CAE45920.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   473 AA;  52121 MW;  9476EAE4C0BFC447 CRC64;

  Query Match           71.4%;  Score 2191.5;  DB 2;  Length 473;
  Best Local Similarity  90.1%;  Pred. No. 1.5e-134;
  Matches  409;  Conservative   21;  Mismatches   19;  Indels    5;  Gaps    1;

Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60
              |:|||||||  ||||||||:||||||| || : |:|||||||||||::||:  |:  ||
Db         20 EIQLVESGGGLVQPGGSLRLSCAASGFTFSSFEMNWVRQAPGKGLEWLSYITRSGNTVYY 79

Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGT-----YYFDSWGQGTLL 115
              :||::|||||||||::|:||||| ||||||:|||:| |     |      :|| |||| |:
Db         80 ADSLQGRFTISRDNARNSLYLQMNSLRAEDTAVYYCARQNEHTSPWYPSFFDYWGQGILV 139

Qy        116 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 175
              ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        140 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFLEPVTVSWNSGALTSGVHTFPAV 199

Qy        176 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE 235
              ||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||
Db        200 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPE 259

Qy        236 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 319

Qy        296 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 379

Qy        356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 415
              ||:|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 439

Qy        416 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||||||||||||||||||
Db        440 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 473
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RESULT 9
CAE45920
ID   CAE45920    PRELIMINARY;      PRT;   473 AA.
AC   CAE45920;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein DKFZp686C11235.
GN   DKFZP686C11235.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Human small intestine;
RA   Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX640853; CAE45920.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   473 AA;  52121 MW;  9476EAE4C0BFC447 CRC64;

  Query Match             71.4%;  Score 2191.5;  DB 2;  Length 473;
  Best Local Similarity   90.1%;  Pred. No. 1.5e-134;
  Matches  409;  Conservative   21;  Mismatches   19;  Indels    5;  Gaps    1;

Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60
              |:|||||||  ||||||||:|||||| || : |:||||||||||||::||:  |:  ||
Db         20 EIQLVESGGGLVQPGGSLRLSCAASGFTFSSFEMNWVRQAPGKGLEWLSYITRSGNTVYY 79

Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGT-----YYFDSWGQGTLL 115
              :||::|||||||||::|:|||||  ||||||:|||:| |     |      :|| |||| |:
Db         80 ADSLQGRFTISRDNARNSLYLQMNSLRAEDTAVYYCARQNEHTSPWYPSFFDYWGQGILV 139

Qy        116 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 175
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        140 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFLEPVTVSWNSGALTSGVHTFPAV 199

Qy        176 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE 235
              ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db        200 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPE 259

Qy        236 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 319

Qy        296 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 379

Qy        356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 415
              ||:|:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 439

Qy        416 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||||||||||||||||||
Db        440 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 473


RESULT 10
BAC85232
ID   BAC85232    PRELIMINARY;      PRT;   472 AA.
AC   BAC85232;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   CDNA FLJ26265 fis, clone DMC05516, highly similar to Ig gamma-1 chain
DE   C region.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Dermoid tumor;
RA   Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y.,
RA   Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
RA   Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
RA   Kawakami B., Nagai K., Isogai T., Sugano S.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK129776; BAC85232.1; -.
SQ   SEQUENCE   472 AA;  51212 MW;  01BF215F99809164 CRC64;

  Query Match             71.3%;  Score 2191;  DB 2;  Length 472;
  Best Local Similarity   90.1%;  Pred. No. 1.6e-134;
  Matches  410;  Conservative   17;  Mismatches   20;  Indels    8;  Gaps    2;

Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60
              || |::|||  |||||||:|||||||   ||:|||| ||||||||: |   | |||
Db         20 EVNLLQSGGGLVQPGGSLRLSCAASGFAFGGTAMTWVRQVPGKGLEWVSAIGGSGYSTYY 79

Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTYY------FDSWGQGTL 114
              :||| ||||:||||| ||:|||| ||| ||:|:|:| : ::|  |      ||:|||||:
Db         80 ADSVTGRFTVSRDNSNNTVYLQMNSLRVEDTAMYYCAKDRVG--YGGNPDSFDAWGQGTM 137

Qy        115 LTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 174
              :|| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 VTVGSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 197

Qy        175 VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP 234
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP 257

Qy        235 ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 294
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 317

Qy        295 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP 354
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP 377

Qy        355 PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV 437

Qy        415 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||||||||||||||||||
Db        438 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 472


RESULT 11
Q6GMW7
ID   Q6GMW7      PRELIMINARY;      PRT;   475 AA.
AC   Q6GMW7;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073782; AAH73782.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   475 AA;  51987 MW;  2A1FE55D736860F8 CRC64;

  Query Match             71.3%;  Score 2188.5;  DB 2;  Length 475;
  Best Local Similarity   91.0%;  Pred. No. 2.3e-134;
  Matches  415;  Conservative   11;  Mismatches   23;  Indels    7;  Gaps    2;

Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60
              |||||||| |||||||:|| || |  | :|| ||||||||||:|: ||:  : |||
Db         20 EVQLVESGGGLVQPGGSLRLSCVASAFTLSRHAMHWVRQAPGKGLEYVSGISNSENSTYY 79

Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVK------LGTYY-FDSWGQGT 113
              :|||||||||||| |||||||: |||||| |||:| | :      |  ||  | |||||
Db         80 ADSVKGRFTISRDNYKNTLYLQLGSLRAEDKAVYYCARARCRGDTCLNFYYGLDVWGQGT 139

Qy        114 LLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 173
               : |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 TVIVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 199

Qy        174 AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA 259

Qy        234 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 319

Qy        294 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 379

Qy        354 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 413
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 439

Qy        414 VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||||||||||||||||||||
Db        440 VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 475


RESULT 12
Q6IN78
ID   Q6IN78      PRELIMINARY;      PRT;   466 AA.
AC   Q6IN78;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   IGHG1 protein.
GN   Name=IGHG1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Peripheral Nervous System;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Peripheral Nervous System;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC072419; AAH72419.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ   SEQUENCE   466 AA;  50853 MW;  53EB0BCEDE81076E CRC64;

  Query Match             71.2%;  Score 2187;  DB 2;  Length 466;
  Best Local Similarity   92.0%;  Pred. No. 2.9e-134;
  Matches  415;  Conservative   11;  Mismatches   19;  Indels    6;  Gaps    3;

Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60
              |||||||| :|||||| :||||||    |   | |||||||||||||: :  ||: |||
Db         20 EVQLVESGGGLIQPGGSLTLSCAASGLTVSSNYMHWVRQAPGKGLEWVSVLYIGGA-TYY 78

Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYFDS--WGQGTLLTVS 118
              :|||||||||||||||||||| |||||:|||:| |  | |   :  ||||||:|||
Db         79 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR---GNYVVPAAPWGQGTLVTVS 135

Qy        119 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 195

Qy        179 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 238
```

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                 ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Db        196 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLG 255

Qy        239 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 298
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 315

Qy        299 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 358
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 375

Qy        359 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 418
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 435

Qy        419 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
                 ||||||||||||||||||||||||||||||
Db        436 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 466


RESULT 13
Q6N089
ID   Q6N089      PRELIMINARY;      PRT;   472 AA.
AC   Q6N089;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein DKFZp686P15220.
GN   Name=DKFZp686P15220;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Human rectum tumor;
RG   THE GERMAN HUMAN CDNA CONSORTIUM;
RA   Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX640627; CAE45781.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   472 AA;  51724 MW;  26CB340D0046D279 CRC64;

  Query Match             71.2%;  Score 2187;  DB 2;  Length 472;
  Best Local Similarity   91.2%;  Pred. No. 2.9e-134;
  Matches  414;  Conservative   13;  Mismatches   21;  Indels    6;  Gaps    3;

Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60
              |||||||||  |||| |||:||||||| |  ||| ||||||||||||: ||       |
Db         20 EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIAY 79

Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGT---YYF--DSWGQGTLL 115
              :|||||||||||| ||:||||| ||||||:|:|:| : ::|    ||:  | ||||| :
Db         80 ADSVKGRFTISRDNGKNSLYLQMNSLRAEDTALYYCAK-EIGAHNFYYYGMDVWGQGTTV 138

Qy        116 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 198

Qy        176 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE 235
                 ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db        199 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPE 258

Qy        236 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 295
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 318

Qy        296 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 355
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 378

Qy        356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 415
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 438

Qy        416 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
                 ||||||||||||||||||||||||||||||||
Db        439 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 472


RESULT 14
CAE45781
ID   CAE45781    PRELIMINARY;      PRT;   472 AA.
AC   CAE45781;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein DKFZp686P15220.
GN   DKFZP686P15220.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Human rectum tumor;
RA   Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX640627; CAE45781.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   472 AA;  51724 MW;  26CB340D0046D279 CRC64;

  Query Match             71.2%;  Score 2187;  DB 2;  Length 472;
  Best Local Similarity   91.2%;  Pred. No. 2.9e-134;
  Matches  414;  Conservative   13;  Mismatches   21;  Indels    6;  Gaps    3;

Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60
              |||||||||  |||| |||:||||||| |  ||| ||||||||||||: ||       |
Db         20 EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIAY 79

Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGT---YYF--DSWGQGTLL 115
              :|||||||||||| ||:||||| ||||||:|:|:| : ::|    ||:  | ||||| :
Db         80 ADSVKGRFTISRDNGKNSLYLQMNSLRAEDTALYYCAK-EIGAHNFYYYGMDVWGQGTTV 138

Qy        116 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 198

Qy        176 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE 235
                 ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db        199 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPE 258

Qy        236 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 295
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 318

Qy        296 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 355
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 378

Qy        356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 415
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        379 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 438

Qy        416 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||||||||||||||||||
Db        439 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 472


RESULT 15
AAH06402
ID   AAH06402    PRELIMINARY;      PRT;   479 AA.
AC   AAH06402;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC006402; AAH06402.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   479 AA;  52281 MW;  D74E0C89082A9788 CRC64;

  Query Match             71.2%;  Score 2185.5;  DB 2;  Length 479;
  Best Local Similarity   90.0%;  Pred. No. 3.7e-134;
  Matches  414;  Conservative   13;  Mismatches   22;  Indels   11;  Gaps    2;

Qy          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60
              |||||||||  |||| |||:|||||||  |  |||  |||| ||||||||: ||       |
Db         20 EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQVPGKGLEWVSGISCNSGSIGY 79

Qy         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTR-VKL----------GTYYFDSW 109
              :|||||||||||:| :|||||  ||||||:|:|:| : ::|          |:  || |
Db         80 ADSVKGRFTISRDNAKKSLYLQMNSLRAEDTALYYCAKDIELDIVVVPAPMRGSLGFDYW 139

Qy        110 GQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV 169
              |||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 GQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV 199

Qy        170 HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP 229
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP 259

Qy        230 PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 289
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 319

Qy        290 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 379

Qy        350 VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY 409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY 439

Qy        410 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||||||||||||||||||||||||||
Db        440 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 479


Search completed: December 23, 2004, 19:04:37
Job time : 163.904 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2004, 18:30:04 ; Search time 28.8913 Seconds
(without alignments)
1340.986 Million cell updates/sec

Title: US-10-089-500-54
Perfect score: 568
Sequence: 1 DIQMTQSPSSLSASVGDRVT.....HQYSKLPWTFGQGTKVEIKR 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	568	100.0	108	4	AAB81988	Aab81988 Gangliosi
2	568	100.0	128	4	AAB81999	Aab81999 Gangliosi
3	562	98.9	108	6	ABU11011	Abu11011 Modified
4	561	98.8	128	4	AAB81994	Aab81994 Gangliosi
5	555	97.7	128	4	AAB81997	Aab81997 Gangliosi
6	551	97.0	128	4	AAB81993	Aab81993 Gangliosi
7	548	96.5	108	4	AAB81986	Aab81986 Gangliosi
8	545	96.0	128	4	AAB81995	Aab81995 Gangliosi
9	545	96.0	128	4	AAB81996	Aab81996 Gangliosi
10	544	95.8	128	4	AAB81998	Aab81998 Gangliosi
11	532	93.7	128	4	AAB81992	Aab81992 Gangliosi
12	514	90.5	108	4	AAB81990	Aab81990 Gangliosi
13	514	90.5	108	6	ABU11013	Abu11013 Modified
14	514	90.5	128	3	AAB01628	Aab01628 Murine im
15	514	90.5	128	4	AAB81978	Aab81978 Gangliosi
16	514	90.5	128	6	ABU11003	Abu11003 Modified
17	513	90.3	128	2	AAR33257	Aar33257 Rat immun
18	507	89.3	110	2	AAW70673	Aaw70673 Anti-VEGF
19	507	89.3	110	5	ABP61242	Abp61242 Humanised
20	507	89.3	237	2	AAW70703	Aaw70703 Protein e
21	507	89.3	650	5	ABP61241	Abp61241 Phage-dis
22	506	89.1	128	2	AAY28368	Aay28368 pKM641 LA
23	505	88.9	107	2	AAW86805	Aaw86805 Variable
24	505	88.9	107	2	AAW70625	Aaw70625 Humanised
25	505	88.9	107	5	ABP61194	Abp61194 Humanised
26	504	88.7	110	2	AAW70675	Aaw70675 Anti-VEGF
27	504	88.7	110	5	ABP61244	Abp61244 Humanised
28	503	88.6	108	2	AAW70618	Aaw70618 Anti-VEGF
29	503	88.6	108	5	ABP61187	Abp61187 Humanised
30	503	88.6	108	8	ADG31782	Adg31782 V(L) doma
31	503	88.6	108	8	ADG31768	Adg31768 V(L) doma
32	503	88.6	108	8	ADG31893	Adg31893 V(L) prot
33	503	88.6	110	3	AAB05897	Aab05897 Humanised
34	503	88.6	110	3	AAB13376	Aab13376 F(ab)-12
35	501	88.2	107	2	AAW86804	Aaw86804 Variable
36	501	88.2	107	2	AAW70623	Aaw70623 Humanised
37	501	88.2	107	5	ABP61192	Abp61192 Humanised
38	500	88.0	108	8	ADG31770	Adg31770 V(L) doma
39	500	88.0	110	2	AAW70677	Aaw70677 Anti-VEGF
40	500	88.0	110	2	AAW70687	Aaw70687 Anti-VEGF
41	500	88.0	110	3	AAB13380	Aab13380 Anti-VEGF
42	500	88.0	110	5	ABP61256	Abp61256 Humanised
43	500	88.0	110	5	ABP61246	Abp61246 Humanised
44	500	88.0	214	7	ADC26154	Adc26154 Parent an
45	500	88.0	237	5	ABB81107	Abb81107 Anti-VEGF

ALIGNMENTS

RESULT 1
AAB81988
ID AAB81988 standard; protein; 108 AA.
XX
AC AAB81988;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 54.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Claim 22; Page 172-173; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 108 AA;

Query Match 100.0%; Score 568; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.2e-35;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108


RESULT 2
AAB81999
ID   AAB81999 standard; protein; 128 AA.
XX
AC   AAB81999;
XX
DT   03-JUL-2001  (first entry)
XX
DE   Ganglioside GD3 specific antibody related protein #8.
XX
KW   Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW   cancer.
XX
OS   Synthetic.
XX
PN   WO200123432-A1.
XX
PD   05-APR-2001.
XX
PF   29-SEP-2000; 2000WO-JP006774.
XX
PR   30-SEP-1999;   99JP-00278291.
PR   06-APR-2000; 2000JP-00105088.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Hanai N,  Shitara K,  Nakamura K,  Niwa R;
XX
DR   WPI; 2001-266143/27.
DR   N-PSDB; AAF86913.
XX
PT   New human type complementation-determining region-transplanted antibody
PT   and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT   of e.g. tumors, with low antigenicity, little side effects but potent
PT   activity in cancer.
XX
PS   Ecample 1; Page 166; 183pp; Japanese.
XX
CC   The present invention describes a monoclonal antibody which can react
CC   specifically with ganglioside GD3. The antibody and its derivatives are
CC   useful in the diagnosis and therapy of tumours, particularly cancer
CC   diagnosis. The present sequence is a protein used in the exemplification
CC   of the invention
XX
SQ   Sequence 128 AA;

  Query Match             100.0%;  Score 568;  DB 4;  Length 128;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-35;
  Matches  108;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 80

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 128


RESULT 3
ABU11011
ID   ABU11011 standard; protein; 108 AA.
XX
AC   ABU11011;
XX
DT   04-FEB-2003  (first entry)
XX
DE   Modified ganglioside GD3 antibody associated protein #4.
XX
KW   Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
XX
OS   Synthetic.
XX
PN   WO200278739-A1.
XX
PD   10-OCT-2002.
XX
PF   29-MAR-2002; 2002WO-JP003170.
XX
PR   29-MAR-2001; 2001JP-00097483.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Shitara K,  Niwa R,  Kanazawa J,  Asada M;
XX
DR   WPI; 2003-067410/06.
XX
PT   Drugs containing genetically-modified antibody against ganglioside GD3,
PT   its fragment, immunocompetent cell activators or/and antitumor agents in
PT   combination, applicable in treating malignant tumor like melanoma.
XX
PS   Claim 8; Page 100; 121pp; Japanese.
XX
CC   The invention describes drugs contain a genetically-modified antibody
CC   against ganglioside GD3 or its fragment and at least 1 of a substance
CC   capable of activating immunocompetent cells and a substance having an
CC   antitumor activity in combination. The drugs can be used to treat tumour
CC   like melanoma and can provide a treatment with enhanced therapeutic
CC   effect and little side-reactions, particularly to relieve problems of
CC   side-effects during the conventional single administration. This sequence
CC   represents a protein associated with the anti- ganglioside GD3 antibody
XX
SQ   Sequence 108 AA;

  Query Match             98.9%;  Score 562;  DB 6;  Length 108;
  Best Local Similarity   99.1%;  Pred. No. 3.4e-35;
  Matches  107;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAPKLLIFYSSNLHSGVPS 60

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108


RESULT 4
AAB81994
ID   AAB81994 standard; protein; 128 AA.
XX
AC   AAB81994;
XX
DT   03-JUL-2001  (first entry)
XX
DE   Ganglioside GD3 specific antibody related protein #3.
XX
KW   Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW   cancer.
XX
OS   Synthetic.
XX
PN   WO200123432-A1.
XX
PD   05-APR-2001.
XX
```

PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
DR N-PSDB; AAF86898.
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Example 1; Page 155-156; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 128 AA;

Query Match 98.8%; Score 561; DB 4; Length 128;
Best Local Similarity 98.1%; Pred. No. 4.7e-35;
Matches 106; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 21 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 80

Qy 61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
|||||||||||||||||||| |||:||||||||||||||||||
Db 81 RFSGGGSGTDYTLTISSLQPEDFATYYCHQYSKLPWTFGQGTKVEIKR 128

RESULT 5
AAB81997
ID AAB81997 standard; protein; 128 AA.
XX
AC AAB81997;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein #6.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
DR N-PSDB; AAF86907.
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Example 1; Page 161-162; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 128 AA;

Query Match 97.7%; Score 555; DB 4; Length 128;
Best Local Similarity 98.1%; Pred. No. 1.3e-34;
Matches 106; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
|||||||||||||||||||||||||||||||||||||||||||| || ||||||||||||||||
Db 21 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPGKAPKLLIFYSSNLHSGVPS 80

Qy 61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 81 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 128

RESULT 6
AAB81993
ID AAB81993 standard; protein; 128 AA.
XX
AC AAB81993;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein #2.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
DR N-PSDB; AAF86895.
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Example 1; Page 153; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 128 AA;

Query Match 97.0%; Score 551; DB 4; Length 128;

```
  Best Local Similarity   97.2%;  Pred. No. 2.7e-34;
  Matches  105;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              ||||||||||||||||||||||||||||||||||||||||||| || ||||||||||||||||
Db         21 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPGKAPKLLIFYSSNLHSGVPS 80

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              ||||||||||||||||||||| |||||||||||||||||||||||||||
Db         81 RFSGGGSGTDYTLTISSLQPEDFATYFCHQYSKLPWTFGQGTKVEIKR 128


RESULT 7
AAB81986
ID   AAB81986 standard; protein; 108 AA.
XX
AC   AAB81986;
XX
DT   03-JUL-2001  (first entry)
XX
DE   Ganglioside GD3 specific antibody related protein SEQ ID NO: 10.
XX
KW   Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW   cancer.
XX
OS   Synthetic.
XX
PN   WO200123432-A1.
XX
PD   05-APR-2001.
XX
PF   29-SEP-2000; 2000WO-JP006774.
XX
PR   30-SEP-1999;   99JP-00278291.
PR   06-APR-2000; 2000JP-00105088.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Hanai N,  Shitara K,  Nakamura K,  Niwa R;
XX
DR   WPI; 2001-266143/27.
XX
PT   New human type complementation-determining region-transplanted antibody
PT   and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT   of e.g. tumors, with low antigenicity, little side effects but potent
PT   activity in cancer.
XX
PS   Example 1; Page 143-144; 183pp; Japanese.
XX
CC   The present invention describes a monoclonal antibody which can react
CC   specifically with ganglioside GD3. The antibody and its derivatives are
CC   useful in the diagnosis and therapy of tumours, particularly cancer
CC   diagnosis. The present sequence is a protein used in the exemplification
CC   of the invention
XX
SQ   Sequence 108 AA;

  Query Match            96.5%;  Score 548;  DB 4;  Length 108;
  Best Local Similarity   96.3%;  Pred. No. 3.9e-34;
  Matches  104;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              ||||||||||||||||||||||||||||||||||||||||| || ||||||||||||||||
Db          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPGKAPKLLIFYSSNLHSGVPS 60

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              ||||||||||||||||||||| |||:||||||||||||||||||||||
Db         61 RFSGGGSGTDYTLTISSLQPEDFATYYCHQYSKLPWTFGQGTKVEIKR 108


RESULT 8
AAB81995
ID   AAB81995 standard; protein; 128 AA.
XX
AC   AAB81995;
XX
DT   03-JUL-2001  (first entry)
XX
DE   Ganglioside GD3 specific antibody related protein #4.
XX
KW   Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW   cancer.
XX
OS   Synthetic.
XX
PN   WO200123432-A1.
XX
PD   05-APR-2001.
XX
PF   29-SEP-2000; 2000WO-JP006774.
XX
PR   30-SEP-1999;   99JP-00278291.
PR   06-APR-2000; 2000JP-00105088.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Hanai N,  Shitara K,  Nakamura K,  Niwa R;
XX
DR   WPI; 2001-266143/27.
DR   N-PSDB; AAF86901.
XX
PT   New human type complementation-determining region-transplanted antibody
PT   and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT   of e.g. tumors, with low antigenicity, little side effects but potent
PT   activity in cancer.
XX
PS   Example 1; Page 157-158; 183pp; Japanese.
XX
CC   The present invention describes a monoclonal antibody which can react
CC   specifically with ganglioside GD3. The antibody and its derivatives are
CC   useful in the diagnosis and therapy of tumours, particularly cancer
CC   diagnosis. The present sequence is a protein used in the exemplification
CC   of the invention
XX
SQ   Sequence 128 AA;

  Query Match            96.0%;  Score 545;  DB 4;  Length 128;
  Best Local Similarity   95.4%;  Pred. No. 7.6e-34;
  Matches  103;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              ||||||||||||||||||||||||||||||||||||||||| || ||||||||||||||||
Db         21 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPGKAPKLLIFYSSNLHSGVPS 80

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              ||||||||||:||||:||||||||||:||||||||||||||||||||||
Db         81 RFSGGGSGTDYSLTISNLQPEDIATYYCHQYSKLPWTFGQGTKVEIKR 128


RESULT 9
AAB81996
ID   AAB81996 standard; protein; 128 AA.
XX
AC   AAB81996;
XX
DT   03-JUL-2001  (first entry)
XX
DE   Ganglioside GD3 specific antibody related protein #5.
XX
KW   Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW   cancer.
XX
OS   Synthetic.
XX
PN   WO200123432-A1.
XX
```

PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
DR N-PSDB; AAF86904.
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Example 1; Page 159-160; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 128 AA;

Query Match 96.0%; Score 545; DB 4; Length 128;
Best Local Similarity 95.4%; Pred. No. 7.6e-34;
Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
||||||||||||||||||||||||||||||||||||||||||| || ||||||||||||||||
Db 21 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPGKAPKLLIFYSSNLHSGVPS 80

Qy 61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
|||||||||||||||:||||| |||:||||||||||||||||||
Db 81 RFSGGGSGTDYTLTISNLQPEDFATYYCHQYSKLPWTFGQGTKVEIKR 128

RESULT 10
AAB81998
ID AAB81998 standard; protein; 128 AA.
XX
AC AAB81998;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein #7.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
DR N-PSDB; AAF86912.
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Example 3; Page 164-165; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 128 AA;

Query Match 95.8%; Score 544; DB 4; Length 128;
Best Local Similarity 96.3%; Pred. No. 9.1e-34;
Matches 104; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
||||||| ||| ||||||||||||||||||||||||||| ||||||||||||||||||
Db 21 DIQMTQSASSLPASVGDRVTITCSASQDISNYLNWYQQKPGKAVKLLIFYSSNLHSGVPS 80

Qy 61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
|||||||||||||||||||||| ||||||||||||||||||||||||
Db 81 RFSGGGSGTDYTLTISSLQPEDFATYFCHQYSKLPWTFGQGTKVEIKR 128

RESULT 11
AAB81992
ID AAB81992 standard; protein; 128 AA.
XX
AC AAB81992;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein #1.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
DR N-PSDB; AAF86892.
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Example 1; Page 150-151; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 128 AA;

```
  Query Match             93.7%;  Score 532;  DB 4;  Length 128;
  Best Local Similarity   93.5%;  Pred. No. 7.3e-33;
  Matches  101;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              ||||||: ||| |||||||||||||||||||||||||| || ||||||||||||||||
Db         21 DIQMTQTASSLPASVGDRVTITCSASQDISNYLNWYQQKPGKAPKLLIFYSSNLHSGVPS 80

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              |||||||||||||||||||| |||:|||||||||||||||||||||
Db         81 RFSGGGSGTDYTLTISSLQPEDFATYYCHQYSKLPWTFGQGTKVEIKR 128


RESULT 12
AAB81990
ID   AAB81990 standard; protein; 108 AA.
XX
AC   AAB81990;
XX
DT   03-JUL-2001  (first entry)
XX
DE   Ganglioside GD3 specific antibody related protein SEQ ID NO: 56.
XX
KW   Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW   cancer.
XX
OS   Mus musculus.
XX
PN   WO200123432-A1.
XX
PD   05-APR-2001.
XX
PF   29-SEP-2000; 2000WO-JP006774.
XX
PR   30-SEP-1999;   99JP-00278291.
PR   06-APR-2000; 2000JP-00105088.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Hanai N,  Shitara K,  Nakamura K,  Niwa R;
XX
DR   WPI; 2001-266143/27.
XX
PT   New human type complementation-determining region-transplanted antibody
PT   and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT   of e.g. tumors, with low antigenicity, little side effects but potent
PT   activity in cancer.
XX
PS   Claim 11; Page 174-175; 183pp; Japanese.
XX
CC   The present invention describes a monoclonal antibody which can react
CC   specifically with ganglioside GD3. The antibody and its derivatives are
CC   useful in the diagnosis and therapy of tumours, particularly cancer
CC   diagnosis. The present sequence is a protein used in the exemplification
CC   of the invention
XX
SQ   Sequence 108 AA;

  Query Match             90.5%;  Score 514;  DB 4;  Length 108;
  Best Local Similarity   88.9%;  Pred. No. 1.4e-31;
  Matches   96;  Conservative    7;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              ||||||: ||| ||:|||||||:|||||||||||||||||  ||||||||||||||||
Db          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              ||||||||||:||||:|:|||||||||||||||||| |||:||||
Db         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108


RESULT 13
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ABU11013
ID   ABU11013 standard; protein; 108 AA.
XX
AC   ABU11013;
XX
DT   04-FEB-2003  (first entry)
XX
DE   Modified ganglioside GD3 antibody associated protein #6.
XX
KW   Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
XX
OS   Mus musculus.
XX
PN   WO200278739-A1.
XX
PD   10-OCT-2002.
XX
PF   29-MAR-2002; 2002WO-JP003170.
XX
PR   29-MAR-2001; 2001JP-00097483.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Shitara K,  Niwa R,  Kanazawa J,  Asada M;
XX
DR   WPI; 2003-067410/06.
XX
PT   Drugs containing genetically-modified antibody against ganglioside GD3,
PT   its fragment, immunocompetent cell activators or/and antitumor agents in
PT   combination, applicable in treating malignant tumor like melanoma.
XX
PS   Claim 7; Page 113; 121pp; Japanese.
XX
CC   The invention describes drugs contain a genetically-modified antibody
CC   against ganglioside GD3 or its fragment and at least 1 of a substance
CC   capable of activating immunocompetent cells and a substance having an
CC   antitumor activity in combination. The drugs can be used to treat tumour
CC   like melanoma and can provide a treatment with enhanced therapeutic
CC   effect and little side-reactions, particularly to relieve problems of
CC   side-effects during the conventional single administration. This sequence
CC   represents a protein associated with the anti- ganglioside GD3 antibody
XX
SQ   Sequence 108 AA;

  Query Match             90.5%;  Score 514;  DB 6;  Length 108;
  Best Local Similarity   88.9%;  Pred. No. 1.4e-31;
  Matches   96;  Conservative    7;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              ||||||: ||| ||:|||||||:|||||||||||||||||  ||||||||||||||||
Db          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              ||||||||||:||||:|:|||||||||||||||||| |||:||||
Db         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108


RESULT 14
AAB01628
ID   AAB01628 standard; protein; 128 AA.
XX
AC   AAB01628;
XX
DT   07-DEC-2000  (first entry)
XX
DE   Murine immunoglobulin light chain variable region.
XX
KW   Mouse; immunoglobulin; L chain; light chain; variable region; cancer;
KW   humanised antibody.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
```

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FT   Peptide         1. .20
FT                   /label= signal_peptide
FT   Protein         21. .128
FT                   /label= mature_immunoglobulin_light_chain_V_region
XX
PN   EP1013761-A2.
XX
PD   28-JUN-2000.
XX
PF   18-SEP-1992;   99EP-00124345.
XX
PR   18-SEP-1991;   91JP-00238375.
PR   18-SEP-1992;   92EP-00116026.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Shitara K,  Hanai N,  Hasegawa M,  Miyaji H,  Kuwana Y;
XX
DR   WPI; 2000-402204/35.
DR   N-PSDB; AAA51004.
XX
PT   New humanized chimera antibody KM-871 useful for treating cancer,
PT   comprises variable region of mouse monoclonal antibody, reactive with
PT   ganglioside and human antibody constant region.
XX
PS   Claim 14; Page 28-29; 65pp; English.
XX
CC   The present sequence is a murine immunoglobulin light chain variable
CC   region from plasmid KM-641. The coding sequence was used in the creation
CC   of an expression vector, along with the sequence for a human antibody, to
CC   produce humanised chimaeric antibodies, which can be used to treat
CC   cancer. Humanised chimaeric antibodies are more effective than mouse
CC   antibodies as they do not provoke a reaction in the human and side
CC   effects, such as the formation of anti-mouse immunoglobulin antibody and
CC   the rapid half-life of the immunoglobulins, do not occur
XX
SQ   Sequence 128 AA;

  Query Match             90.5%;  Score 514;  DB 3;  Length 128;
  Best Local Similarity   88.9%;  Pred. No. 1.7e-31;
  Matches   96;  Conservative    7;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              ||||||: ||| ||:||||||:||||||||||||||||||  ||||||||||||||||
Db         21 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 80

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              ||||||||||:||||:|:||||||||||||||||||| |||:||||
Db         81 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 128


RESULT 15
AAB81978
ID   AAB81978 standard; protein; 128 AA.
XX
AC   AAB81978;
XX
DT   03-JUL-2001  (first entry)
XX
DE   Ganglioside GD3 specific antibody related protein SEQ ID NO: 2.
XX
KW   Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW   cancer.
XX
OS   Mus musculus.
XX
PN   WO200123432-A1.
XX
PD   05-APR-2001.
XX
PF   29-SEP-2000; 2000WO-JP006774.
XX
PR   30-SEP-1999;   99JP-00278291.
PR   06-APR-2000; 2000JP-00105088.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Hanai N,  Shitara K,  Nakamura K,  Niwa R;
XX
DR   WPI; 2001-266143/27.
XX
PT   New human type complementation-determining region-transplanted antibody
PT   and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT   of e.g. tumors, with low antigenicity, little side effects but potent
PT   activity in cancer.
XX
PS   Example 1; Page 140; 183pp; Japanese.
XX
CC   The present invention describes a monoclonal antibody which can react
CC   specifically with ganglioside GD3. The antibody and its derivatives are
CC   useful in the diagnosis and therapy of tumours, particularly cancer
CC   diagnosis. The present sequence is a protein used in the exemplification
CC   of the invention
XX
SQ   Sequence 128 AA;

  Query Match             90.5%;  Score 514;  DB 4;  Length 128;
  Best Local Similarity   88.9%;  Pred. No. 1.7e-31;
  Matches   96;  Conservative    7;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              ||||||: ||| ||:||||||:||||||||||||||||||  ||||||||||||||||
Db         21 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 80

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              ||||||||||:||||:|:||||||||||||||||||| |||:||||
Db         81 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 128


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Job time : 29.8913 secs
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OM protein - protein search, using sw model

Run on: December 23, 2004, 18:46:39 ; Search time 7.13276 Seconds
(without alignments)
1004.148 Million cell updates/sec

Title: US-10-089-500-54
Perfect score: 568
Sequence: 1 DIQMTQSPSSLSASVGDRVT.....HQYSKLPWTFGQGTKVEIKR 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	514	90.5	128	4	US-09-225-322B-10	Sequence 10, Appl
2	514	90.5	128	4	US-09-225-322B-19	Sequence 19, Appl
3	514	90.5	128	4	US-09-764-304-10	Sequence 10, Appl
4	514	90.5	128	4	US-09-764-304-19	Sequence 19, Appl
5	503	88.6	110	4	US-09-440-781-94	Sequence 94, Appl
6	491	86.4	108	3	US-09-065-059-3	Sequence 3, Appli
7	487	85.7	127	3	US-08-649-100-33	Sequence 33, Appl
8	484	85.2	214	1	US-08-458-516-12	Sequence 12, Appl
9	481	84.7	110	4	US-09-440-781-95	Sequence 95, Appl
10	480	84.5	107	2	US-07-934-373C-17	Sequence 17, Appl
11	480	84.5	107	2	US-08-652-558-2	Sequence 2, Appli
12	480	84.5	107	3	US-08-437-642B-17	Sequence 17, Appl
13	480	84.5	107	4	US-08-146-206C-17	Sequence 17, Appl
14	480	84.5	107	4	US-09-705-686-17	Sequence 17, Appl
15	480	84.5	107	4	US-09-705-392A-17	Sequence 17, Appl
16	480	84.5	107	5	PCT-US93-07832-17	Sequence 17, Appl
17	480	84.5	109	2	US-07-934-373C-47	Sequence 47, Appl
18	480	84.5	109	3	US-08-437-642B-47	Sequence 47, Appl
19	480	84.5	214	2	US-07-934-373C-40	Sequence 40, Appl
20	480	84.5	214	2	US-08-788-800-11	Sequence 11, Appl
21	480	84.5	214	3	US-08-437-642B-40	Sequence 40, Appl
22	480	84.5	214	3	US-09-097-309-2	Sequence 2, Appli
23	480	84.5	214	3	US-09-097-171A-2	Sequence 2, Appli
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27	480	84.5	233	2	US-07-934-373C-25	Sequence 25, Appl
28	480	84.5	233	3	US-08-437-642B-25	Sequence 25, Appl
29	480	84.5	233	4	US-08-146-206C-25	Sequence 25, Appl
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31	480	84.5	233	4	US-09-705-392A-25	Sequence 25, Appl
32	480	84.5	233	5	PCT-US93-07832-25	Sequence 25, Appl
33	480	84.5	237	3	US-09-097-309-6	Sequence 6, Appli
34	480	84.5	237	3	US-09-097-171A-10	Sequence 10, Appl
35	480	84.5	237	3	US-09-422-712B-2	Sequence 2, Appli
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39	479	84.3	107	1	US-08-458-516-8	Sequence 8, Appli
40	476	83.8	107	3	US-09-254-189-1	Sequence 1, Appli
41	475	83.6	108	3	US-08-974-899-3	Sequence 3, Appli
42	475	83.6	108	4	US-09-795-798-3	Sequence 3, Appli
43	475	83.6	111	1	US-08-137-117D-67	Sequence 67, Appl
44	475	83.6	111	2	US-08-436-717-67	Sequence 67, Appl
45	475	83.6	126	1	US-08-137-117D-71	Sequence 71, Appl

ALIGNMENTS

RESULT 1
US-09-225-322B-10
; Sequence 10, Application US/09225322B
; Patent No. 6437098
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/225,322B
; CURRENT FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-09-225-322B-10

Query Match 90.5%; Score 514; DB 4; Length 128;
Best Local Similarity 88.9%; Pred. No. 1.2e-43;
Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

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Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              |||||: ||| ||:||||||:||||||||||||||||  ||||||||||||||||
Db         21 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 80

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
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Db         81 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 128
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RESULT 2
US-09-225-322B-19
; Sequence 19, Application US/09225322B

; Patent No. 6437098
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/225,322B
; CURRENT FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:light chain
; OTHER INFORMATION: variable region
US-09-225-322B-19

Query Match 90.5%; Score 514; DB 4; Length 128;
Best Local Similarity 88.9%; Pred. No. 1.2e-43;
Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

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Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              |||||||||||:||||:|:|||||||||||||||||| |||:||||
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RESULT 3
US-09-764-304-10
; Sequence 10, Application US/09764304
; Patent No. 6495666
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; CURRENT FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cDNA KM-641
US-09-764-304-10

Query Match 90.5%; Score 514; DB 4; Length 128;
Best Local Similarity 88.9%; Pred. No. 1.2e-43;
Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

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Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              |||||| ||| ||:|||||||:||||||||||||||||||  ||||||||||||||||
Db         21 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 80

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              |||||||||||:||||:|:|||||||||||||||||| |||:||||
Db         81 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 128
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RESULT 4
US-09-764-304-19
; Sequence 19, Application US/09764304
; Patent No. 6495666
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; CURRENT FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: light chain
; OTHER INFORMATION: variable region
US-09-764-304-19

Query Match 90.5%; Score 514; DB 4; Length 128;
Best Local Similarity 88.9%; Pred. No. 1.2e-43;
Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

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Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
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RESULT 5
US-09-440-781-94

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; Sequence 94, Application US/09440781
; Patent No. 6632926
; GENERAL INFORMATION:
;  APPLICANT: Yvonne Man-yee Chen et al.
;  TITLE OF INVENTION: ANTIBODY VARIANTS
;  FILE REFERENCE: P1469R1
;  CURRENT APPLICATION NUMBER: US/09/440,781
;  CURRENT FILING DATE: 1999-11-16
;  NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 94
;   LENGTH: 110
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   NAME/KEY: artificial
;   LOCATION: 1-110
;   OTHER INFORMATION: humanized antibody light chain variable domain
US-09-440-781-94

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Db          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPGKAPKVLIYFTSSLHSGVPS 60

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              |||| |||||:||||||||||| |||:| ||| :|||||||||||||
Db         61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYSTVPWTFGQGTKVEIKR 108


RESULT 6
US-09-065-059-3
; Sequence 3, Application US/09065059
; Patent No. 6068841
;  GENERAL INFORMATION:
;    APPLICANT:  SEINO, Ken-ichiro
;    APPLICANT:  KAYAGAKI, No. 6068841uhiko
;    APPLICANT:  YAGITA, Hideo
;    APPLICANT:  OKUMURA, Ko
;    APPLICANT:  NAKATA, Motomi
;    TITLE OF INVENTION:  THERAPEUTIC AGENT FOR HEPATITIS
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McDermott, Will & Emery
;      STREET:  99 Canal Center Plaza
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  USA
;      ZIP:  22314
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/065,059
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bucca Ph.D., Daniel
;      REGISTRATION NUMBER:  P-42,368
;      REFERENCE/DOCKET NUMBER:  50356-151
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-518-5100
;      TELEFAX:  703-684-1124
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  108 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-065-059-3

  Query Match             86.4%;  Score 491;  DB 3;  Length 108;
  Best Local Similarity   84.3%;  Pred. No. 1.9e-41;
  Matches   91;  Conservative    9;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              |||||||||||||:||||||:| |||||||||||||||||  |||||:|:| |||||||
Db          1 DIQMTQSPSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 60

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              |||| ||||||:||||:|:||||||||| |||: ||||| |||:||||
Db         61 RFSGSGSGTDYSLTISNLEPEDIATYFCQQYSEFPWTFGGGTKLEIKR 108


RESULT 7
US-08-649-100-33
; Sequence 33, Application US/08649100
; Patent No. 6114507
;  GENERAL INFORMATION:
;    APPLICANT:  SHIRAKAWA, KAMON
;    APPLICANT:  MATUSUE, TOMOKAZU
;    APPLICANT:  NAGATA, SHIGEKAZU
;    APPLICANT:  CO, MAN SUNG
;    APPLICANT:  VASQUEZ, MAXIMILIANO
;    TITLE OF INVENTION:  ANTI-FAS LIGAND ANTIBODY AND ASSAY
;    TITLE OF INVENTION:  METHOD USING THE ANTI-FAS LIGAND ANTIBODY
;    NUMBER OF SEQUENCES:  41
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BIRCH, STEWART, KOLASCH AND BIRCH
;      STREET:  PO BOX 747
;      CITY:  FALLS CHURCH
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22040-0747
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/649,100
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURPHY JR, GERALD M
;      REGISTRATION NUMBER:  28,977
;      REFERENCE/DOCKET NUMBER:  1110-160
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 205-8000
;      TELEFAX:  (703) 205-8050
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  127 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-649-100-33

  Query Match             85.7%;  Score 487;  DB 3;  Length 127;
  Best Local Similarity   86.0%;  Pred. No. 5.6e-41;
  Matches   92;  Conservative    6;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              |||||||||:|||||||||||||| |||||||||||||||| || ||||:|:| |||||||
Db         21 DIQMTQSPSTLSASVGDRVTITCRASQDISNYLNWYQQKPGKAPKLLIYYTSRLHSGVPS 80

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIK 107
              |||| ||||:||||||||||:| ||||| | | |||||||||||:|
Db         81 RFSGSGSGTNYTLTISSLQPDDFATYFCQQGSTLPWTFGQGTKVEVK 127
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```
RESULT 8
US-08-458-516-12
; Sequence 12, Application US/08458516
; Patent No. 5777085
;  GENERAL INFORMATION:
;    APPLICANT:  Co, Man Sung
;    APPLICANT:  Tso, J. Yun
;    TITLE OF INVENTION:  Humanized Antibodies Reactive with
;    TITLE OF INVENTION:  GPIIB/IIIA
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  William M. Smith
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/458,516
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/059,159
;      FILING DATE:  03-MAY-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11823-37-3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-326-2400
;      TELEFAX:  415-326-2422
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  214 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-458-516-12

  Query Match             85.2%;  Score 484;  DB 1;  Length 214;
  Best Local Similarity   83.3%;  Pred. No. 2e-40;
  Matches   90;  Conservative    9;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              ||||||:||:||||||||||:| |||||:|||||||||| || ||||:|:| |||||||
Db          1 DIQMTQTPSTLSASVGDRVTISCRASQDINNYLNWYQQKPGKAPKLLIYYTSTLHSGVPS 60

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              |||| |||||||||||||||:| ||||| | : |||||||||||||:||
Db         61 RFSGSGSGTDYTLTISSLQPDDFATYFCQQGNTLPWTFGQGTKVEVKR 108


RESULT 9
US-09-440-781-95
; Sequence 95, Application US/09440781
; Patent No. 6632926
; GENERAL INFORMATION:
;  APPLICANT: Yvonne Man-yee Chen et al.
;  TITLE OF INVENTION: ANTIBODY VARIANTS
;  FILE REFERENCE: P1469R1
;  CURRENT APPLICATION NUMBER: US/09/440,781
;  CURRENT FILING DATE: 1999-11-16
;  NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 95
;   LENGTH: 110
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   NAME/KEY: artificial
;   LOCATION: 1-110
;   OTHER INFORMATION: humanized antibody light chain variable domain
US-09-440-781-95

  Query Match             84.7%;  Score 481;  DB 4;  Length 110;
  Best Local Similarity   81.5%;  Pred. No. 1.9e-40;
  Matches   88;  Conservative   12;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              |||:||||||||||||||||||| |:: :|||||||||| || |:||:::|:|||||||
Db          1 DIQLTQSPSSLSASVGDRVTITCRANEQLSNYLNWYQQKPGKAPKVLIYFTSSLHSGVPS 60

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              |||| |||||:|||||||||| |||:| ||| :|||||||||||||
Db         61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYSTVPWTFGQGTKVEIKR 108


RESULT 10
US-07-934-373C-17
; Sequence 17, Application US/07934373C
; Patent No. 5821337
;  GENERAL INFORMATION:
;    APPLICANT:  Paul J. Carter
;    APPLICANT:  Leonard G. Presta
;    TITLE OF INVENTION:  Immunoglobulin Variants
;    NUMBER OF SEQUENCES:  48
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/934,373C
;      FILING DATE:  21-Aug-1992
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/05126
;      FILING DATE:  15-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/715272
;      FILING DATE:  14-JUN-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lee, Wendy M.
;      REGISTRATION NUMBER:  40,378
;      REFERENCE/DOCKET NUMBER:  P0709P2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-1994
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-07-934-373C-17

  Query Match             84.5%;  Score 480;  DB 2;  Length 107;
  Best Local Similarity   86.0%;  Pred. No. 2.3e-40;
  Matches   92;  Conservative    4;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              |||||||||||||||||||||||| |||||| |||||||||| || ||||:|:| | |||||
Db          1 DIQMTQSPSSLSASVGDRVTITCRASQDIRNYLNWYQQKPGKAPKLLIYYTSRLESGVPS 60
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Qy          61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIK 107
               |||| |||||||||||||||||| |||:| | : |||||||||||||||
Db          61 RFSGSGSGTDYTLTISSLQPEDFATYYCQQGNTLPWTFGQGTKVEIK 107


RESULT 11
US-08-652-558-2
; Sequence 2, Application US/08652558
; Patent No. 5861155
;  GENERAL INFORMATION:
;    APPLICANT:  LIN, AUGUSTINE YEE-THARN
;    TITLE OF INVENTION:  HUMANIZED ANTIBODIES AND USES
;    TITLE OF INVENTION:  THEREOF
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER & WITCOFF
;      STREET:  75 STATE STREET, 23RD FLOOR
;      CITY:  BOSTON
;      STATE:  MASSACHUSETTS
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette, 1.4 Mb storage
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,558
;      FILING DATE:  JUNE 6, 1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/IB94/00387
;      FILING DATE:  NOVEMBER 21, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  YANKWICH, LEON R.
;      REGISTRATION NUMBER:  30,237
;      REFERENCE/DOCKET NUMBER:  95,497-L
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-345-9100
;      TELEFAX:  617-345-9111
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-652-558-2

  Query Match             84.5%;  Score 480;  DB 2;  Length 107;
  Best Local Similarity   86.8%;  Pred. No. 2.3e-40;
  Matches   92;  Conservative    6;  Mismatches    8;  Indels    0;  Gaps    0;

Qy           1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
               |||||||||||||||||||||||||| |||||||||| | || ||||:|:|:|||||||
Db           1 DIQMTQSPSSLSASVGDRVTITCSASQGISNYLNWYQQTPGKAPKLLIYYTSSLHSGVPS 60

Qy          61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEI 106
               |||| ||||||| |||||||||||||:| |||||| |||||||::|
Db          61 RFSGSGSGTDYTFTISSLQPEDIATYYCQQYSKLPRTFGQGTKLQI 106


RESULT 12
US-08-437-642B-17
; Sequence 17, Application US/08437642B
; Patent No. 6054297
;  GENERAL INFORMATION:
;    APPLICANT:  Paul J. Carter
;    APPLICANT:  Leonard G. Presta
;    TITLE OF INVENTION:  Immunoglobulin Variants
;    NUMBER OF SEQUENCES:  47
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/437,642B
;      FILING DATE:  09-May-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/934373
;      FILING DATE:  21-AUG-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/146206
;      FILING DATE:  17-NOV-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/05126
;      FILING DATE:  15-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/715272
;      FILING DATE:  14-JUN-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lee, Wendy M.
;      REGISTRATION NUMBER:  40,378
;      REFERENCE/DOCKET NUMBER:  P0709P2C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-1994
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-437-642B-17

  Query Match             84.5%;  Score 480;  DB 3;  Length 107;
  Best Local Similarity   86.0%;  Pred. No. 2.3e-40;
  Matches   92;  Conservative    4;  Mismatches   11;  Indels    0;  Gaps    0;

Qy           1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
               |||||||||||||||||||||||||| ||||| |||||||||| || ||||:|:| | |||||
Db           1 DIQMTQSPSSLSASVGDRVTITCRASQDIRNYLNWYQQKPGKAPKLLIYYTSRLESGVPS 60

Qy          61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIK 107
               |||| |||||||||||||||| |||:| | : |||||||||||||||
Db          61 RFSGSGSGTDYTLTISSLQPEDFATYYCQQGNTLPWTFGQGTKVEIK 107


RESULT 13
US-08-146-206C-17
; Sequence 17, Application US/08146206C
; Patent No. 6407213
;  GENERAL INFORMATION:
;    APPLICANT:  Carter, Paul J.
;    APPLICANT:  Presta, Leonard G.
;    TITLE OF INVENTION:  Method for Making Humanized Antibodies
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/146,206C
;      FILING DATE:  17-No. 6407213-1993
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/715272
;      FILING DATE:  14-JUN-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lee, Wendy M.
;      REGISTRATION NUMBER:  40,378
;      REFERENCE/DOCKET NUMBER:  P0709P1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-1994
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-146-206C-17

  Query Match             84.5%;  Score 480;  DB 4;  Length 107;
  Best Local Similarity   86.0%;  Pred. No. 2.3e-40;
  Matches   92;  Conservative    4;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              ||||||||||||||||||||||| ||||| |||||||||| || ||||:|:| | |||||
Db          1 DIQMTQSPSSLSASVGDRVTITCRASQDIRNYLNWYQQKPGKAPKLLIYYTSRLESGVPS 60

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIK 107
              |||| |||||||||||||||| |||:| | : |||||||||||||
Db         61 RFSGSGSGTDYTLTISSLQPEDFATYYCQQGNTLPWTFGQGTKVEIK 107


RESULT 14
US-09-705-686-17
; Sequence 17, Application US/09705686
; Patent No. 6639055
;   GENERAL INFORMATION:
;        APPLICANT: Carter, Paul J.
;                   Presta, Leonard G.
;        TITLE OF INVENTION: Method for Making Humanized Antibodies
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Genentech, Inc.
;             STREET: 1 DNA Way
;             CITY: South San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94080
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: WinPatin (Genentech)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/705,686
;             FILING DATE: 02-No. 6639055-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/146206
;             FILING DATE: 17-NOV-1993
;             APPLICATION NUMBER: 07/715272
;             FILING DATE: 14-JUN-1991
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Lee, Wendy M.
;             REGISTRATION NUMBER: 40,378
;             REFERENCE/DOCKET NUMBER: P0709P1D3
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650/225-1994
;             TELEFAX: 650/952-9881
;   INFORMATION FOR SEQ ID NO: 17:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 107 amino acids
;             TYPE: Amino Acid
;             TOPOLOGY: Linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-705-686-17

  Query Match             84.5%;  Score 480;  DB 4;  Length 107;
  Best Local Similarity   86.0%;  Pred. No. 2.3e-40;
  Matches   92;  Conservative    4;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              ||||||||||||||||||||||| ||||| |||||||||| || ||||:|:| | |||||
Db          1 DIQMTQSPSSLSASVGDRVTITCRASQDIRNYLNWYQQKPGKAPKLLIYYTSRLESGVPS 60

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIK 107
              |||| |||||||||||||||| |||:| | : |||||||||||||
Db         61 RFSGSGSGTDYTLTISSLQPEDFATYYCQQGNTLPWTFGQGTKVEIK 107


RESULT 15
US-09-705-392A-17
; Sequence 17, Application US/09705392A
; Patent No. 6719971
;   GENERAL INFORMATION:
;        APPLICANT: Carter, Paul J.
;                   Presta, Leonard G.
;        TITLE OF INVENTION: Method for Making Humanized Antibodies
;        NUMBER OF SEQUENCES: 36
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Genentech, Inc.
;             STREET: 1 DNA Way
;             CITY: South San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94080
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: WinPatin (Genentech)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/705,392A
;             FILING DATE: 02-No. 6719971-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/146206
;             FILING DATE: 17-NOV-1993
;             APPLICATION NUMBER: 07/715272
;             FILING DATE: 14-JUN-1991
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Lee, Wendy M.
;             REGISTRATION NUMBER: 40,378
;             REFERENCE/DOCKET NUMBER: P0709P1D1 REVISED
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650/225-1994
;             TELEFAX: 650/952-9881
;   INFORMATION FOR SEQ ID NO: 17:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 107 amino acids
;             TYPE: Amino Acid
;             TOPOLOGY: Linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-705-392A-17

  Query Match             84.5%;  Score 480;  DB 4;  Length 107;
  Best Local Similarity   86.0%;  Pred. No. 2.3e-40;
  Matches   92;  Conservative    4;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              ||||||||||||||||||||||| ||||| |||||||||| || ||||:|:| | |||||
Db          1 DIQMTQSPSSLSASVGDRVTITCRASQDIRNYLNWYQQKPGKAPKLLIYYTSRLESGVPS 60

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIK 107
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                ||||| |||||||||||||||||| |||:| | : ||||||||||||||
Db          61 RFSGSGSGTDYTLTISSLQPEDFATYYCQQGNTLPWTFGQGTKVEIK 107
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Search completed: December 23, 2004, 19:08:00
Job time : 17.1328 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2004, 19:04:51 ; Search time 24.5684 Seconds
(without alignments)
1578.640 Million cell updates/sec

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Perfect score: 568
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1595201 seqs, 359116952 residues

Total number of hits satisfying chosen parameters: 1595201

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	514	90.5	128	9	US-09-764-304-19	Sequence 19, Appl
3	514	90.5	128	14	US-10-265-713-10	Sequence 10, Appl
4	514	90.5	128	14	US-10-265-713-19	Sequence 19, Appl
5	514	90.5	128	14	US-10-166-626-10	Sequence 10, Appl
6	514	90.5	128	14	US-10-166-626-19	Sequence 19, Appl
7	507	89.3	110	9	US-09-056-160B-103	Sequence 103, App
8	507	89.3	110	14	US-10-234-671-101	Sequence 101, App
9	507	89.3	237	9	US-09-056-160B-100	Sequence 100, App
10	507	89.3	237	14	US-10-234-671-100	Sequence 100, App
11	507	89.3	491	13	US-10-011-125-2	Sequence 2, Appli
12	505	88.9	107	9	US-09-056-160B-15	Sequence 15, Appl
13	505	88.9	107	14	US-10-234-671-15	Sequence 15, Appl
14	504	88.7	110	9	US-09-056-160B-105	Sequence 105, App
15	504	88.7	110	14	US-10-234-671-103	Sequence 103, App
16	503	88.6	108	9	US-09-056-160B-8	Sequence 8, Appli
17	503	88.6	108	13	US-10-153-159-2	Sequence 2, Appli
18	503	88.6	108	13	US-10-153-159-16	Sequence 16, Appl
19	503	88.6	108	14	US-10-153-176-2	Sequence 2, Appli
20	503	88.6	108	14	US-10-153-176-16	Sequence 16, Appl
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22	503	88.6	108	15	US-10-443-134A-16	Sequence 16, Appl
23	503	88.6	108	15	US-10-443-134A-127	Sequence 127, App
24	503	88.6	110	14	US-10-234-671-8	Sequence 8, Appli
25	503	88.6	110	15	US-10-624-153-94	Sequence 94, Appl
26	503	88.6	667	17	US-10-764-428-25	Sequence 25, Appl
27	501	88.2	107	9	US-09-056-160B-13	Sequence 13, Appl
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43	500	88.0	670	17	US-10-764-428-5	Sequence 5, Appli
44	500	88.0	670	17	US-10-764-428-9	Sequence 9, Appli
45	500	88.0	670	17	US-10-764-428-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-09-764-304-10
; Sequence 10, Application US/09764304
; Patent No. US20020026036A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; CURRENT FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cDNA KM-641
US-09-764-304-10

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RESULT 2
US-09-764-304-19
; Sequence 19, Application US/09764304
; Patent No. US20020026036A1
; GENERAL INFORMATION:
;  APPLICANT: SHITARA, KENYA
;  APPLICANT: HANAI, NOBUO
;  APPLICANT: HASEGAWA, MAMORU
;  APPLICANT: MIYAJI, HIROMASA
;  APPLICANT: KUWANA, YOSHIHISA
;  TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
;  FILE REFERENCE: 249-101
;  CURRENT APPLICATION NUMBER: US/09/764,304
;  CURRENT FILING DATE: 2001-01-19
;  EARLIER APPLICATION NUMBER: 09/225,322
;  EARLIER FILING DATE: 1999-01-05
;  EARLIER APPLICATION NUMBER: US 08/454,680
;  EARLIER FILING DATE: 1995-05-31
;  EARLIER APPLICATION NUMBER: US 08/408,133
;  EARLIER FILING DATE: 1995-03-21
;  EARLIER APPLICATION NUMBER: US 08/292,178
;  EARLIER FILING DATE: 1994-08-17
;  EARLIER APPLICATION NUMBER: US07/947,674
;  EARLIER FILING DATE: 1992-09-17
;  EARLIER APPLICATION NUMBER: JP 3-238375
;  EARLIER FILING DATE: 1991-09-18
;  NUMBER OF SEQ ID NOS: 19
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; SEQ ID NO 19
;   LENGTH: 128
;   TYPE: PRT
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;   FEATURE:
;   OTHER INFORMATION: light chain
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US-09-764-304-19

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; Sequence 10, Application US/10265713
; Publication No. US20030095964A1
; GENERAL INFORMATION:
;  APPLICANT: SHITARA, KENYA
;  APPLICANT:  HANAI, NOBUO
;  APPLICANT:  HASEGAWA, MAMORU
;  APPLICANT:  MIYAJI, HIROMASA
;  APPLICANT:  KUWANA, YOSHIHISA
;  TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
;  FILE REFERENCE: 249-101
;  CURRENT APPLICATION NUMBER: US/10/265,713
;  CURRENT FILING DATE:  2002-10-08
;  PRIOR APPLICATION NUMBER: US/09/225,322
;  PRIOR FILING DATE: 1999-01-05
;  PRIOR APPLICATION NUMBER: US 08/454,680
;  PRIOR FILING DATE: 1995-05-31
;  PRIOR APPLICATION NUMBER: US 08/408,133
;  PRIOR FILING DATE: 1995-03-21
;  PRIOR APPLICATION NUMBER: US 08/292,178
;  PRIOR FILING DATE: 1994-08-17
;  PRIOR APPLICATION NUMBER: US07/947,674
;  PRIOR FILING DATE: 1992-09-17
;  PRIOR APPLICATION NUMBER: JP 3-238375
;  PRIOR FILING DATE: 1991-09-18
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;   LENGTH: 128
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;   OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-10-265-713-10

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; GENERAL INFORMATION:
;  APPLICANT: SHITARA, KENYA
;  APPLICANT:  HANAI, NOBUO
;  APPLICANT:  HASEGAWA, MAMORU
;  APPLICANT:  MIYAJI, HIROMASA
;  APPLICANT:  KUWANA, YOSHIHISA
;  TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
;  FILE REFERENCE: 249-101
;  CURRENT APPLICATION NUMBER: US/10/265,713
;  CURRENT FILING DATE:  2002-10-08
;  PRIOR APPLICATION NUMBER: US/09/225,322
;  PRIOR FILING DATE: 1999-01-05
;  PRIOR APPLICATION NUMBER: US 08/454,680
;  PRIOR FILING DATE: 1995-05-31
;  PRIOR APPLICATION NUMBER: US 08/408,133
;  PRIOR FILING DATE: 1995-03-21
;  PRIOR APPLICATION NUMBER: US 08/292,178
;  PRIOR FILING DATE: 1994-08-17
;  PRIOR APPLICATION NUMBER: US07/947,674
;  PRIOR FILING DATE: 1992-09-17
;  PRIOR APPLICATION NUMBER: JP 3-238375
;  PRIOR FILING DATE: 1991-09-18
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;   OTHER INFORMATION: variable region
US-10-265-713-19

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; Publication No. US20030166876A1
; GENERAL INFORMATION:
;  APPLICANT: SHITARA, KENYA
;  APPLICANT:  HANAI, NOBUO
;  APPLICANT:  HASEGAWA, MAMORU
;  APPLICANT:  MIYAJI, HIROMASA
;  APPLICANT:  KUWANA, YOSHIHISA
;  TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
;  FILE REFERENCE: 249-101
;  CURRENT APPLICATION NUMBER: US/10/166,626
;  CURRENT FILING DATE:  2002-06-12
;  PRIOR APPLICATION NUMBER: US/09/225,322B
;  PRIOR FILING DATE: 1999-01-05
;  PRIOR APPLICATION NUMBER: US 08/454,680
;  PRIOR FILING DATE: 1995-05-31
;  PRIOR APPLICATION NUMBER: US 08/408,133
;  PRIOR FILING DATE: 1995-03-21
;  PRIOR APPLICATION NUMBER: US 08/292,178
;  PRIOR FILING DATE: 1994-08-17
;  PRIOR APPLICATION NUMBER: US07/947,674
;  PRIOR FILING DATE: 1992-09-17
;  PRIOR APPLICATION NUMBER: JP 3-238375
;  PRIOR FILING DATE: 1991-09-18
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.0
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;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-10-166-626-10

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RESULT 6
US-10-166-626-19
; Sequence 19, Application US/10166626
; Publication No. US20030166876A1
; GENERAL INFORMATION:
;  APPLICANT: SHITARA, KENYA
;  APPLICANT:  HANAI, NOBUO
;  APPLICANT:  HASEGAWA, MAMORU
;  APPLICANT:  MIYAJI, HIROMASA
;  APPLICANT:  KUWANA, YOSHIHISA
;  TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
;  FILE REFERENCE: 249-101
;  CURRENT APPLICATION NUMBER: US/10/166,626
;  CURRENT FILING DATE:  2002-06-12
;  PRIOR APPLICATION NUMBER: US/09/225,322B
;  PRIOR FILING DATE: 1999-01-05
;  PRIOR APPLICATION NUMBER: US 08/454,680
;  PRIOR FILING DATE: 1995-05-31
;  PRIOR APPLICATION NUMBER: US 08/408,133
;  PRIOR FILING DATE: 1995-03-21
;  PRIOR APPLICATION NUMBER: US 08/292,178
;  PRIOR FILING DATE: 1994-08-17
;  PRIOR APPLICATION NUMBER: US07/947,674
;  PRIOR FILING DATE: 1992-09-17
;  PRIOR APPLICATION NUMBER: JP 3-238375
;  PRIOR FILING DATE: 1991-09-18
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
;   LENGTH: 128
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:light chain
;   OTHER INFORMATION: variable region
US-10-166-626-19

  Query Match             90.5%;  Score 514;  DB 14;  Length 128;
  Best Local Similarity   88.9%;  Pred. No. 7.1e-37;
  Matches   96;  Conservative    7;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
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RESULT 7
US-09-056-160B-103
; Sequence 103, Application US/09056160B
; Patent No. US20020032315A1
;  GENERAL INFORMATION:
;    APPLICANT:  Baca, Manuel
;    APPLICANT:  Wells, James A.
;    APPLICANT:  Presta, Leonard G.
;    APPLICANT:  Lowman, Henry B.
;    APPLICANT:  Chen, Yvonne M.
;    TITLE OF INVENTION:  ANTI-VEGF ANTIBODIES
;    NUMBER OF SEQUENCES:  131
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/056,160B
;      FILING DATE:  06-Apr-1998
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/054,856
;      FILING DATE:  06-AUG-1997
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;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  P1093R2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-1896
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  103:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  110 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-09-056-160B-103

  Query Match             89.3%;  Score 507;  DB 9;  Length 110;
  Best Local Similarity   88.0%;  Pred. No. 2.5e-36;
  Matches   95;  Conservative    7;  Mismatches    6;  Indels    0;  Gaps    0;

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RESULT 8
US-10-234-671-101
; Sequence 101, Application US/10234671
; Publication No. US20030190317A1
;  GENERAL INFORMATION:
;       APPLICANT: Baca, Manuel
;                  Wells, James A.
;                  Presta, Leonard G.
;                  Lowman, Henry B.
;                  Chen, Yvonne M.
;       TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
;       NUMBER OF SEQUENCES: 131
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Genentech, Inc.
;            STREET: 1 DNA Way
;            CITY: South San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94080
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: WinPatin (Genentech)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/234,671
;            FILING DATE: 03-Sep-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/056160
;            FILING DATE: 06-APR-1998
;            APPLICATION NUMBER: 60/126446
;            FILING DATE: 07-APR-1997
;            APPLICATION NUMBER: 60/054856
;            FILING DATE: 06-AUG-1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Cui, Steven X.
;            REGISTRATION NUMBER: 44,637
;            REFERENCE/DOCKET NUMBER: P1093R2C1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 650/225-8674
;            TELEFAX: 650/952-9881
;   INFORMATION FOR SEQ ID NO: 101:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 110 amino acids
;            TYPE: Amino Acid
;            TOPOLOGY: Linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 101:
US-10-234-671-101

  Query Match             89.3%;  Score 507;  DB 14;  Length 110;
  Best Local Similarity   88.0%;  Pred. No. 2.5e-36;
  Matches   95;  Conservative    7;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              |||:|||||||||||||||||||||||||||||||||| || ||||:::|:|||||||
Db          1 DIQLTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPGKAPKLLIYFTSSLHSGVPS 60

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              |||| |||||||||||||||| |||:| ||| :|||||||||||||||
Db         61 RFSGSGSGTDYTLTISSLQPEDFATYYCQQYSTVPWTFGQGTKVEIKR 108


RESULT 9
US-09-056-160B-100
; Sequence 100, Application US/09056160B
; Patent No. US20020032315A1
;  GENERAL INFORMATION:
;    APPLICANT:  Baca, Manuel
;    APPLICANT:  Wells, James A.
;    APPLICANT:  Presta, Leonard G.
;    APPLICANT:  Lowman, Henry B.
;    APPLICANT:  Chen, Yvonne M.
;    TITLE OF INVENTION:  ANTI-VEGF ANTIBODIES
;    NUMBER OF SEQUENCES:  131
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/056,160B
;      FILING DATE:  06-Apr-1998
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/054,856
;      FILING DATE:  06-AUG-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  P1093R2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-1896
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  100:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  237 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-09-056-160B-100

  Query Match             89.3%;  Score 507;  DB 9;  Length 237;
  Best Local Similarity   88.0%;  Pred. No. 5.3e-36;
  Matches   95;  Conservative    7;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              |||:|||||||||||||||||||||||||||||||||| || ||||:::|:|||||||
Db         24 DIQLTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPGKAPKLLIYFTSSLHSGVPS 83

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              |||| |||||||||||||||| |||:| ||| :|||||||||||||||
Db         84 RFSGSGSGTDYTLTISSLQPEDFATYYCQQYSTVPWTFGQGTKVEIKR 131
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```
RESULT 10
US-10-234-671-100
; Sequence 100, Application US/10234671
; Publication No. US20030190317A1
;   GENERAL INFORMATION:
;        APPLICANT: Baca, Manuel
;                   Wells, James A.
;                   Presta, Leonard G.
;                   Lowman, Henry B.
;                   Chen, Yvonne M.
;        TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
;        NUMBER OF SEQUENCES: 131
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Genentech, Inc.
;             STREET: 1 DNA Way
;             CITY: South San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94080
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: WinPatin (Genentech)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/234,671
;             FILING DATE: 03-Sep-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/056160
;             FILING DATE: 06-APR-1998
;             APPLICATION NUMBER: 60/126446
;             FILING DATE: 07-APR-1997
;             APPLICATION NUMBER: 60/054856
;             FILING DATE: 06-AUG-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Cui, Steven X.
;             REGISTRATION NUMBER: 44,637
;             REFERENCE/DOCKET NUMBER: P1093R2C1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650/225-8674
;             TELEFAX: 650/952-9881
;   INFORMATION FOR SEQ ID NO: 100:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 237 amino acids
;             TYPE: Amino Acid
;             TOPOLOGY: Linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-234-671-100

  Query Match             89.3%;  Score 507;  DB 14;  Length 237;
  Best Local Similarity   88.0%;  Pred. No. 5.3e-36;
  Matches   95;  Conservative    7;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              |||:|||||||||||||||||||||||||||||||||| || ||||:::|:|||||||
Db         24 DIQLTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPGKAPKLLIYFTSSLHSGVPS 83

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              |||| |||||||||||||||| |||:| ||| :|||||||||||||||
Db         84 RFSGSGSGTDYTLTISSLQPEDFATYYCQQYSTVPWTFGQGTKVEIKR 131


RESULT 11
US-10-011-125-2
; Sequence 2, Application US/10011125
; Publication No. US20020142388A1
; GENERAL INFORMATION:
;  APPLICANT: Chen, Christina Yu-Ching
;  TITLE OF INVENTION: BACTERIAL HOST STRAINS
;  FILE REFERENCE: P1804R1
;  CURRENT APPLICATION NUMBER: US/10/011,125
;  CURRENT FILING DATE:  2001-12-07
;  PRIOR APPLICATION NUMBER: US 60/256,162
;  PRIOR FILING DATE: 2000-12-14
;  NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 2
;   LENGTH: 491
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Sequence is synthesized.
US-10-011-125-2

  Query Match             89.3%;  Score 507;  DB 13;  Length 491;
  Best Local Similarity   88.0%;  Pred. No. 1.1e-35;
  Matches   95;  Conservative    7;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              |||:|||||||||||||||||||||||||||||||||| || ||||:::|:|||||||
Db         24 DIQLTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPGKAPKLLIYFTSSLHSGVPS 83

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              |||| |||||||||||||||| |||:| ||| :|||||||||||||||
Db         84 RFSGSGSGTDYTLTISSLQPEDFATYYCQQYSTVPWTFGQGTKVEIKR 131


RESULT 12
US-09-056-160B-15
; Sequence 15, Application US/09056160B
; Patent No. US20020032315A1
;  GENERAL INFORMATION:
;    APPLICANT:  Baca, Manuel
;    APPLICANT:  Wells, James A.
;    APPLICANT:  Presta, Leonard G.
;    APPLICANT:  Lowman, Henry B.
;    APPLICANT:  Chen, Yvonne M.
;    TITLE OF INVENTION:  ANTI-VEGF ANTIBODIES
;    NUMBER OF SEQUENCES:  131
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/056,160B
;      FILING DATE:  06-Apr-1998
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/054,856
;      FILING DATE:  06-AUG-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  P1093R2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-1896
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-09-056-160B-15

  Query Match             88.9%;  Score 505;  DB 9;  Length 107;
  Best Local Similarity   88.8%;  Pred. No. 3.6e-36;
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  Matches   95;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              ||||||||||||||||||||||||||||||||||||||||| || ||||:::|:|||||||
Db          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPGKAPKLLIYFTSSLHSGVPS 60

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIK 107
              |||| |||||||||||||||| |||:| ||| :|||||||||||||
Db         61 RFSGSGSGTDYTLTISSLQPEDFATYYCQQYSTVPWTFGQGTKVEIK 107


RESULT 13
US-10-234-671-15
; Sequence 15, Application US/10234671
; Publication No. US20030190317A1
;   GENERAL INFORMATION:
;        APPLICANT: Baca, Manuel
;                   Wells, James A.
;                   Presta, Leonard G.
;                   Lowman, Henry B.
;                   Chen, Yvonne M.
;        TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
;        NUMBER OF SEQUENCES: 131
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Genentech, Inc.
;             STREET: 1 DNA Way
;             CITY: South San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94080
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: WinPatin (Genentech)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/234,671
;             FILING DATE: 03-Sep-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/056160
;             FILING DATE: 06-APR-1998
;             APPLICATION NUMBER: 60/126446
;             FILING DATE: 07-APR-1997
;             APPLICATION NUMBER: 60/054856
;             FILING DATE: 06-AUG-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Cui, Steven X.
;             REGISTRATION NUMBER: 44,637
;             REFERENCE/DOCKET NUMBER: P1093R2C1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650/225-8674
;             TELEFAX: 650/952-9881
;   INFORMATION FOR SEQ ID NO: 15:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 107 amino acids
;             TYPE: Amino Acid
;             TOPOLOGY: Linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-234-671-15

  Query Match             88.9%;  Score 505;  DB 14;  Length 107;
  Best Local Similarity   88.8%;  Pred. No. 3.6e-36;
  Matches   95;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              ||||||||||||||||||||||||||||||||||||||||| || ||||:::|:|||||||
Db          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPGKAPKLLIYFTSSLHSGVPS 60

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIK 107
              |||| |||||||||||||||| |||:| ||| :|||||||||||||
Db         61 RFSGSGSGTDYTLTISSLQPEDFATYYCQQYSTVPWTFGQGTKVEIK 107


RESULT 14
US-09-056-160B-105
; Sequence 105, Application US/09056160B
; Patent No. US20020032315A1
;  GENERAL INFORMATION:
;    APPLICANT:  Baca, Manuel
;    APPLICANT:  Wells, James A.
;    APPLICANT:  Presta, Leonard G.
;    APPLICANT:  Lowman, Henry B.
;    APPLICANT:  Chen, Yvonne M.
;    TITLE OF INVENTION:  ANTI-VEGF ANTIBODIES
;    NUMBER OF SEQUENCES:  131
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/056,160B
;      FILING DATE:  06-Apr-1998
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/054,856
;      FILING DATE:  06-AUG-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  P1093R2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-1896
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  105:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  110 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-09-056-160B-105

  Query Match             88.7%;  Score 504;  DB 9;  Length 110;
  Best Local Similarity   87.0%;  Pred. No. 4.5e-36;
  Matches   94;  Conservative    8;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              |||:|||||||||||||||||||||||||||||||||| || |:||:::|:|||||||
Db          1 DIQLTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPGKAPKVLIYFTSSLHSGVPS 60

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              |||| |||||||||||||||| |||:| ||| :|||||||||||||||
Db         61 RFSGSGSGTDYTLTISSLQPEDFATYYCQQYSTVPWTFGQGTKVEIKR 108


RESULT 15
US-10-234-671-103
; Sequence 103, Application US/10234671
; Publication No. US20030190317A1
;   GENERAL INFORMATION:
;        APPLICANT: Baca, Manuel
;                   Wells, James A.
;                   Presta, Leonard G.
;                   Lowman, Henry B.
;                   Chen, Yvonne M.
;        TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
;        NUMBER OF SEQUENCES: 131
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Genentech, Inc.
```

```
;             STREET: 1 DNA Way
;             CITY: South San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94080
;       COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: WinPatin (Genentech)
;       CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/234,671
;             FILING DATE: 03-Sep-2002
;             CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/056160
;             FILING DATE: 06-APR-1998
;             APPLICATION NUMBER: 60/126446
;             FILING DATE: 07-APR-1997
;             APPLICATION NUMBER: 60/054856
;             FILING DATE: 06-AUG-1997
;       ATTORNEY/AGENT INFORMATION:
;             NAME: Cui, Steven X.
;             REGISTRATION NUMBER: 44,637
;             REFERENCE/DOCKET NUMBER: P1093R2C1
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650/225-8674
;             TELEFAX: 650/952-9881
;   INFORMATION FOR SEQ ID NO: 103:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 110 amino acids
;             TYPE: Amino Acid
;             TOPOLOGY: Linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 103:
US-10-234-671-103

  Query Match             88.7%;  Score 504;  DB 14;  Length 110;
  Best Local Similarity   87.0%;  Pred. No. 4.5e-36;
  Matches   94;  Conservative    8;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              |||:||||||||||||||||||||||||||||||||| || |:||:::|:|||||||
Db          1 DIQLTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPGKAPKVLIYFTSSLHSGVPS 60

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              |||| |||||||||||||||| |||:| ||| :|||||||||||||||
Db         61 RFSGSGSGTDYTLTISSLQPEDFATYYCQQYSTVPWTFGQGTKVEIKR 108


Search completed: December 23, 2004, 19:35:47
Job time : 25.5684 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2004, 18:46:03 ; Search time 5.83589 Seconds
(without alignments)
1780.604 Million cell updates/sec

Title: US-10-089-500-54
Perfect score: 568
Sequence: 1 DIQMTQSPSSLSASVGDRVT.....HQYSKLPWTFGQGTKVEIKR 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	480	84.5	108	1	K1HUAU	Ig kappa chain V-I
2	479	84.3	111	2	A38740	Ig kappa chain V r
3	477	84.0	111	2	E38740	Ig kappa chain V r
4	472	83.1	111	2	G38740	Ig kappa chain V r
5	469	82.6	111	2	C38740	Ig kappa chain V r
6	466	82.0	107	2	B49026	Ig kappa chain V r
7	462	81.3	127	2	S40367	Ig kappa chain V-J
8	461	81.2	108	1	KVMS73	Ig kappa chain V r
9	461	81.2	108	2	S69900	Ig kappa chain (cl
10	456	80.3	108	1	K1HURE	Ig kappa chain V-I
11	454	79.9	122	2	A29380	Ig kappa chain pre
12	452	79.6	108	2	S69903	Ig kappa chain (cl
13	452	79.6	115	2	JL0080	Ig kappa chain pre
14	451	79.4	129	2	S52789	Ig kappa chain V r
15	450	79.2	110	2	S44118	Ig kappa chain V-J
16	448	78.9	108	1	KVMSAR	Ig kappa chain V r
17	447	78.7	108	2	S69902	Ig kappa chain (cl
18	447	78.7	109	2	PH0888	Ig kappa chain V r
19	447	78.7	126	2	A34904	Ig kappa chain pre
20	445	78.3	108	1	K1HUAG	Ig kappa chain V-I
21	445	78.3	108	2	I39154	Ig kappa chain (BR
22	445	78.3	125	2	S40333	Ig kappa chain V-J
23	444	78.2	128	2	A26406	Ig kappa chain V r
24	443.5	78.1	107	2	S69901	Ig kappa chain (cl
25	443	78.0	139	2	S40365	Ig kappa chain - h
26	442	77.8	123	2	S40331	Ig kappa chain - h
27	442	77.8	131	2	S40352	Ig kappa chain V-J
28	441.5	77.7	108	2	S38862	Ig kappa chain V r
29	441	77.6	108	2	B49047	Ig kappa chain V r
30	440	77.5	107	2	A48677	Ig kappa chain V-J
31	439	77.3	108	2	S44122	Ig kappa chain V r
32	439	77.3	108	2	C26405	Ig kappa chain V r
33	438	77.1	108	1	K1HURY	Ig kappa chain V-I
34	438	77.1	108	2	S19970	Ig kappa chain V r
35	437.5	77.0	107	2	S36275	Ig lambda chain V
36	437	76.9	107	2	B48677	Ig kappa chain V-J
37	437	76.9	107	2	B28044	Ig kappa chain V r
38	436	76.8	108	2	PL0282	Ig kappa chain V r
39	435	76.6	109	2	S31998	Ig kappa chain - h
40	434	76.4	107	2	S36264	Ig lambda chain V
41	434	76.4	107	2	A28044	Ig kappa chain V r
42	433	76.2	107	2	D48677	Ig kappa chain V-J
43	433	76.2	108	1	K1HUWE	Ig kappa chain V-I
44	433	76.2	108	2	B26405	Ig kappa chain V r
45	433	76.2	127	2	PH1224	Ig kappa chain pre

ALIGNMENTS

RESULT 1
K1HUAU
Ig kappa chain V-I region (Au) - human
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004
C;Accession: A91653; A01862; S02573
R;Schiechl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 353, 345-370, 1972
A;Title: Die Primaerstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, Su
A;Reference number: A91653; MUID:72189444; PMID:5028201
A;Accession: A91653
A;Molecule type: protein
A;Residues: 1-108 <SCH>
A;Cross-references: UNIPROT:P01594
A;Note: the C region of this chain has the Inv (3) marker
R;Fehlhammer, H.; Schiffer, M.; Epp, O.; Colman, P.M.; Lattman, E.E.; Schwager, P.; Ste
Biophys. Struct. Mech. 1, 139-146, 1975
A;Title: The structure determination of the variable portion of the Bence-Jones protein
A;Reference number: A90729; MUID:77022433; PMID:1234024
A;Contents: annotation; X-ray crystallography
A;Note: the structure of the V region was determined by molecular replacement methods u
R;Steiner, V.; Chang, J.Y.
FEBS Lett. 222, 6-10, 1987
A;Title: Chemical modification of the carboxyl groups of protein substrates enhances th
A;Reference number: S02572; MUID:88005152; PMID:3115831
A;Contents: annotation
C;Comment: This is a Bence Jones protein.
C;Genetics:
A;Gene: GDB:IGKV1
A;Cross-references: GDB:136264
A;Map position: 2p12-2p12
C;Complex: an immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into l
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status predicted

Query Match 84.5%; Score 480; DB 1; Length 108;
Best Local Similarity 85.2%; Pred. No. 1.7e-36;
Matches 92; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

```
Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              |||||||||||||||||||||| |||||:||||||||| || ||||: :||| |||||
Db          1 DIQMTQSPSSLSASVGDRVTITCQASQDISDYLNWYQQKPGKAPKLLIYDASNLESGVPS 60

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              ||||||||  :| |||||||||||||:| ||  ||||||||||||||
Db         61 RFSGGGSGAHFTFTISSLQPEDIATYYCQQYDYLPWTFGQGTKVEIKR 108
```

RESULT 2

```
A38740
Ig kappa chain V region (Py20) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004
C;Accession: A38740
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequences and antibody properties of anti
A;Reference number: A38740; MUID:91177923; PMID:1706720
A;Accession: A38740
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: mRNA
A;Residues: 1-111 <RUF>
A;Cross-references: UNIPROT:Q91WS9
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-93/Domain: immunoglobulin homology <IMM>

  Query Match             84.3%;  Score 479;  DB 2;  Length 111;
  Best Local Similarity   80.6%;  Pred. No. 2.2e-36;
  Matches   87;  Conservative   14;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              |:|||: |||||:||||||:||||| ||||||||||||  |||||:|:|:|||||||
Db          4 DVQMTQTTSSLSASLGDRVTISCSASQGISNYLNWYQQKPDGTVKLLIYYTSSLHSGVPS 63

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              |||| ||||||:||||:|:|||:|||:| ||||:||||| |||:||||
Db         64 RFSGSGSGTDYSLTISNLEPEDVATYYCQQYSKVPWTFGGGTKLEIKR 111


RESULT 3
E38740
Ig kappa chain V region (Py54) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004
C;Accession: E38740
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequences and antibody properties of anti
A;Reference number: A38740; MUID:91177923; PMID:1706720
A;Accession: E38740
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: mRNA
A;Residues: 1-111 <RUF>
A;Cross-references: UNIPROT:Q91WS9
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-93/Domain: immunoglobulin homology <IMM>

  Query Match             84.0%;  Score 477;  DB 2;  Length 111;
  Best Local Similarity   81.5%;  Pred. No. 3.3e-36;
  Matches   88;  Conservative   11;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              |: |||: |||||:||||||:||||| ||||||||||||  |||||:|:|:|||||||
Db          4 DVMMTQTTSSLSASLGDRVTISCSASQGISNYLNWYQQKPDGTVKLLIYYTSSLHSGVPS 63

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              |||| ||||||:|||| |:|||||||:| ||||||||| |||:||||
Db         64 RFSGSGSGTDYSLTISDLEPEDIATYYCQQYSKLPWTFGGGTKLEIKR 111


RESULT 4
G38740
Ig kappa chain V region (Py69) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004
C;Accession: G38740
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequences and antibody properties of anti
A;Reference number: A38740; MUID:91177923; PMID:1706720
A;Accession: G38740
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: mRNA
A;Residues: 1-111 <RUF>
A;Cross-references: UNIPROT:Q91WS9
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-93/Domain: immunoglobulin homology <IMM>

  Query Match             83.1%;  Score 472;  DB 2;  Length 111;
  Best Local Similarity   81.5%;  Pred. No. 9.4e-36;
  Matches   88;  Conservative   10;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              |: |||| |||||:|||||:||||||| ||||||||||  |||||:|:|:||| |||
Db          4 DVLMTQSTSSLSASLGDRVTISCSASQDIRNYLNWYQQKPDGTVKLLIYYTSSLHSEVPS 63

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              |||| |||||:|||| |:||||||:| ||||||||| |||:||||
Db         64 RFSGSGSGTDYSLTISDLEPEDIATYYCQQYSKLPWTFGGGTKLEIKR 111


RESULT 5
C38740
Ig kappa chain V region (Py2) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004
C;Accession: C38740
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequences and antibody properties of anti
A;Reference number: A38740; MUID:91177923; PMID:1706720
A;Accession: C38740
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: mRNA
A;Residues: 1-111 <RUF>
A;Cross-references: UNIPROT:Q91WS9
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-93/Domain: immunoglobulin homology <IMM>

  Query Match             82.6%;  Score 469;  DB 2;  Length 111;
  Best Local Similarity   78.7%;  Pred. No. 1.8e-35;
  Matches   85;  Conservative   14;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              |: |||: |||||:|||||:||||| ||||||||| |||  |||||:|:|:|||||||
Db          4 DVMMTQTTSSLSASLGDRVTISCSASQGISNYLNWYQHKPDGTVKLLIYYTSSLHSGVPS 63

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              |||| |||||:|||:|:|||:|||:| ||||:||||| |||:||||
Db         64 RFSGSGSGTDYSLTISNLEPEDVATYYCQQYSKVPWTFGGGTKLEIKR 111


RESULT 6
B49026
Ig kappa chain V region, anti-idiotypic monoclonal antibody - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Accession: B49026; PL0220
R;Koizumi, T.; Puccetti, A.; Migliorini, P.; Barrett, K.J.; Schwartz, R.S.
Eur. J. Immunol. 21, 2185-2193, 1991
A;Title: Molecular heterogeneity of auto-anti-idiotypic antibodies in MLR-lpr/lpr mice.
A;Reference number: A49026; MUID:91364791; PMID:1909645
A;Accession: B49026
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-107 <KOI>
A;Experimental source: MLR-lpr/lpr
A;Note: sequence extracted from NCBI backbone (NCBIP:60876)
R;Puccetti, A.; Koizumi, T.; Migliorini, P.; Andre-Schwartz, J.; Barrett, K.J.; Schwartz
J. Exp. Med. 171, 1919-1930, 1990
A;Title: An immunoglobulin light chain from a lupus-prone mouse induces autoantibodies
```

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A;Reference number: PL0220; MUID:90278348; PMID:1693654
A;Accession: PL0220
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-107 <PUC>
A;Experimental source: strain lupus-prone MRL-lpr/lpr mouse
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;50-56/Region: complementarity-determining 2
F;89-97/Region: complementarity-determining 3

  Query Match             82.0%;  Score 466;  DB 2;  Length 107;
  Best Local Similarity   82.2%;  Pred. No. 3.1e-35;
  Matches   88;  Conservative   10;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              ||||||: |||||||:|||||||:| |||||||||||||||||  |||||:|:| |||||||
Db          1 DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 60

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIK 107
              |||| |||||||:||||:|:|||||||:| |||||| ||| |||:|||
Db         61 RFSGSGSGTDYSLTISNLEPEDIATYYCQQYSKLPRTFGGGTKLEIK 107


RESULT 7
S40367
Ig kappa chain V-J-C region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40367
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40367
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-127 <KLE>
A;Cross-references: EMBL:X72477
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>

  Query Match             81.3%;  Score 462;  DB 2;  Length 127;
  Best Local Similarity   82.4%;  Pred. No. 8.6e-35;
  Matches   89;  Conservative    6;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              ||||||||||||||||||||||| ||| |||||||||:|| || |||| : :|:| |||||
Db         18 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQRKPGKAPKLLIYAASSLQSGVPS 77

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              |||| |||||:|||||||||||| |||:| |    ||||||||||||||
Db         78 RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYNTPWTFGQGTKVEIKR 125


RESULT 8
KVMS73
Ig kappa chain V region (MOPC 173) - mouse (tentative sequence)
C;Species: Mus musculus (house mouse)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C;Accession: A01926
R;Schiff, C.; Fougereau, M.
Eur. J. Biochem. 59, 525-537, 1975
A;Title: Determination of the primary structure of a mouse IgG2a immunoglobulin. Amino-a
A;Reference number: A01926; MUID:76091934; PMID:812696
A;Accession: A01926
A;Molecule type: protein
A;Residues: 1-108 <SCH>
A;Cross-references: UNIPROT:P01643
C;Comment: This chain was isolated from a myeloma protein.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into l
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status predicted

  Query Match             81.2%;  Score 461;  DB 1;  Length 108;
  Best Local Similarity   78.7%;  Pred. No. 9e-35;
  Matches   85;  Conservative   13;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              ||||||: |||||||:|||||||:||||| | |||:|||||||  |||||:|:|:|||||||
Db          1 DIQMTQTTSSLSASLGDRVTISCSASQSIGNYLBWYQQKPDGTVKLLIYYTSSLHSGVPS 60

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              |||| |||||||:|||| |:|::||||:| |||||| ||| |||:||||
Db         61 RFSGSGSGTDYSLTISBLZPZBIATYYCQQYSKLPRTFGGGTKLEIKR 108


RESULT 9
S69900
Ig kappa chain (clone KL2.18 / KL4B10 / KL4C11) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C;Accession: S69900; S69907; S69908
R;Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.
Immunology 75, 116-121, 1992
A;Title: B-cell proliferation initiated by Ia cross-linking and sustained by interleuki
A;Reference number: S69900; MUID:92165291; PMID:1537587
A;Accession: S69900
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-108 <WYS>
A;Cross-references: EMBL:X55041; NID:g511023; PIDN:CAA38881.1; PID:g511024
A;Accession: S69907
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-108 <WY2>
A;Cross-references: EMBL:X55048; NID:g511037; PIDN:CAA38888.1; PID:g511038
A;Accession: S69908
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-108 <WY3>
A;Cross-references: EMBL:X55049; NID:g511039; PIDN:CAA38889.1; PID:g511040
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

  Query Match             81.2%;  Score 461;  DB 2;  Length 108;
  Best Local Similarity   80.6%;  Pred. No. 9e-35;
  Matches   87;  Conservative   10;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              ||||||: |||||||:|||||||:| |||||||||||||||  |||||:|:| |||||||
Db          1 DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 60

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              |||| ||||||:||||:|: |||||||| | : |||||| |||:||||
Db         61 RFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPWTFGGGTKLEIKR 108


RESULT 10
K1HURE
Ig kappa chain V-I region (Rei) - human (tentative sequence)
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C;Accession: A91663; A01873
R;Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 356, 167-191, 1975
A;Title: Die Primaerstruktur einer kristallinen monoklonalen Immunglobulin-L-Kette vom
 vollstaendige Aminosaeuresequenz des Proteins.
A;Reference number: A91663; MUID:76023758; PMID:809329
A;Accession: A91663
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A;Molecule type: protein
A;Residues: 1-108 <PAL>
A;Cross-references: UNIPROT:P01607
A;Note: the C region of this chain has the Inv (1,2) marker
R;Epp, O.; Lattman, E.E.; Schiffer, M.; Huber, R.; Palm, W.
Biochemistry 14, 4943-4952, 1975
A;Title: The molecular structure of a dimer composed of the variable portions of the Ben
A;Reference number: A90392; MUID:76039968; PMID:1182131
A;Contents: annotation; X-ray crystallography, 2.0 angstroms
C;Comment: This is a Bence Jones protein.
C;Genetics:
A;Gene: GDB:IGKV1
A;Cross-references: GDB:136264
A;Map position: 2p12-2p12
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status experimental

  Query Match             80.3%;  Score 456;  DB 1;  Length 108;
  Best Local Similarity   80.6%;  Pred. No. 2.5e-34;
  Matches   87;  Conservative    7;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              |||||||||||||||||||||||| |||||  ||||||| | || |||| : :||| :||||
Db          1 DIQMTQSPSSLSASVGDRVTITCQASQDIIKYLNWYQQTPGKAPKLLIYEASNLQAGVPS 60

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              |||| ||||||| |||||||||||||:| ||  ||:|||||||::| |
Db         61 RFSGSGSGTDYTFTISSLQPEDIATYYCQQYQSLPYTFGQGTKLQITR 108


RESULT 11
A29380
Ig kappa chain precursor V region (AC-1001) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 21-Jan-2000
C;Accession: A29380
R;Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.
J. Biol. Chem. 262, 13579-13583, 1987
A;Title: Nucleotide and translated amino acid sequences of cDNA coding for the variable
A;Reference number: A92612; MUID:88007582; PMID:3115981
A;Accession: A29380
A;Molecule type: mRNA
A;Residues: 1-122 <CHE>
A;Cross-references: GB:M17160; GB:J02815; NID:g196895; PIDN:AAA38824.1; PID:g196896
A;Note: the authors translated the codon TTC for residue 1 as Leu
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;30-104/Domain: immunoglobulin homology <IMM>

  Query Match             79.9%;  Score 454;  DB 2;  Length 122;
  Best Local Similarity   79.6%;  Pred. No. 4.3e-34;
  Matches   86;  Conservative   10;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              ||||||: |||||:||||||:| |||||:|||||||||||  ||||| |:| |||||||
Db         15 DIQMTQTTSSLSASLGDRVTISCRASQDINNYLNWYQQKPDGTVKLLIHYTSRLHSGVPS 74

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              |||| ||||||:||||:|: |||||||| | : |||||| |||:||||
Db         75 RFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPWTFGGGTKLEIKR 122


RESULT 12
S69903
Ig kappa chain (clone KL2.29 / KL2.33 / KL3.8) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C;Accession: S69903; S69904; S69905
R;Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.
Immunology 75, 116-121, 1992
A;Title: B-cell proliferation initiated by Ia cross-linking and sustained by interleukin
A;Reference number: S69900; MUID:92165291; PMID:1537587
A;Accession: S69903
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-108 <WYS>
A;Cross-references: EMBL:X55044; NID:g511029; PIDN:CAA38884.1; PID:g511030
A;Accession: S69904
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-108 <WY2>
A;Cross-references: EMBL:X55045; NID:g511031; PIDN:CAA38885.1; PID:g511032
A;Accession: S69905
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-108 <WY3>
A;Cross-references: EMBL:X55046; NID:g511033; PIDN:CAA38886.1; PID:g511034
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

  Query Match             79.6%;  Score 452;  DB 2;  Length 108;
  Best Local Similarity   79.6%;  Pred. No. 5.8e-34;
  Matches   86;  Conservative   11;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              ||||||: |||||:||||||:| |||||||||||||||||  |||||:|:| |||||||
Db          1 DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 60

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              |||| |||||||:||||:|: |||||||| | : ||:||| |||:||||
Db         61 RFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGTKLEIKR 108


RESULT 13
JL0080
Ig kappa chain precursor V region (anti-phenyloxazolone, 18C10) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jan-2000
C;Accession: JL0080
R;Kaartinen, M.; Rocca-Serra, J.; Maekelae, O.
Mol. Immunol. 25, 859-865, 1988
A;Title: Combinatorial association of V genes: one VH gene codes for three non-cross-re
A;Reference number: JL0076; MUID:89096973; PMID:3211160
A;Accession: JL0080
A;Molecule type: mRNA
A;Residues: 1-115 <KAA>
A;Cross-references: GB:M27793; NID:g197161; PIDN:AAA38937.1; PID:g197162
A;Note: the authors translated the codon AGG for residue 30 as Ser
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-6/Domain: signal sequence (fragment) #status predicted <SIG>
F;7-115/Product: Ig light chain #status predicted <MAT>
F;22-96/Domain: immunoglobulin homology <IMM>
F;30-40/Region: complementarity-determining 1
F;56-62/Region: complementarity-determining 2

  Query Match             79.6%;  Score 452;  DB 2;  Length 115;
  Best Local Similarity   79.6%;  Pred. No. 6.2e-34;
  Matches   86;  Conservative   11;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              ||||||: |||||:||||||:| |||||||||||||||||  |||||:|:| |||||||
Db          7 DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 66

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              |||| |||||||:||||:|: |||||||| | : ||:||| |||:||||
Db         67 RFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGTKLEIKR 114


RESULT 14
S52789
Ig kappa chain V region - human (fragment)
```

```
C;Species: Homo sapiens (man)
C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S52789
R;Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougenot, B.; Ronco, P.; Denoroy, L.; Deret,
submitted to the EMBL Data Library, March 1995
A;Description: Light chain V region gene usage restriction and peculiarities in myeloma-
A;Reference number: S52789
A;Accession: S52789
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-129 <ROC>
A;Cross-references: EMBL:X85995; NID:g758588; PIDN:CAA59987.1; PID:g758589
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;38-112/Domain: immunoglobulin homology <IMM>

  Query Match             79.4%;  Score 451;  DB 2;  Length 129;
  Best Local Similarity   81.3%;  Pred. No. 8.6e-34;
  Matches   87;  Conservative    7;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              |||||||||||||||||||||| |||||||||||||||| || ||||  :|:| :||||
Db         23 DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIHAASSLETGVPS 82

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIK 107
              |||| |||||:: |||||||||:|||:| ||  || ||| |||||||
Db         83 RFSGSGSGTDFSFTISSLQPEDLATYYCQQYDNLPLTFGGGTKVEIK 129


RESULT 15
S44118
Ig kappa chain V-J region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Accession: S44118
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r
A;Reference number: S44105
A;Accession: S44118
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-110 <HAW>
A;Cross-references: EMBL:Z31395; NID:g472972; PIDN:CAA83270.1; PID:g940529
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

  Query Match             79.2%;  Score 450;  DB 2;  Length 110;
  Best Local Similarity   80.9%;  Pred. No. 8.9e-34;
  Matches   89;  Conservative    6;  Mismatches   13;  Indels    2;  Gaps    1;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              |||||||||||||||||| || |||||||||||||||| || ||||: :||| :||||
Db          1 DIQMTQSPSSLSASVGDRVTSTCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPS 60

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLP--WTFGQGTKVEIKR 108
              |||| |||||:| ||||||||||||:| ||  ||   ||| ||||:|||
Db         61 RFSGSGSGTDFTFTISSLQPEDIATYYCQQYDNLPPGVTFGPGTKVDIKR 110


Search completed: December 23, 2004, 19:06:05
Job time : 6.83589 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2004, 18:31:20 ; Search time 30.044 Seconds
(without alignments)
2068.313 Million cell updates/sec

Title: US-10-089-500-54
Perfect score: 568
Sequence: 1 DIQMTQSPSSLSASVGDRVT.....HQYSKLPWTFGQGTKVEIKR 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	480	84.5	108	1	KV1B_HUMAN	P01594 homo sapien
2	465	81.9	233	2	Q91WS9	Q91ws9 mus musculu
3	461	81.2	108	1	KV5J_MOUSE	P01643 mus musculu
4	461	81.2	234	2	Q8R062	Q8r062 mus musculu
5	456	80.3	108	1	KV1O_HUMAN	P01607 homo sapien
6	454	79.9	111	2	AAR10992	Aar10992 mus muscu
7	448	78.9	108	1	KV5K_MOUSE	P01644 mus musculu
8	447	78.7	108	1	KV5L_MOUSE	P01645 mus musculu
9	447	78.7	108	1	KV5M_MOUSE	P01646 mus musculu
10	445	78.3	108	1	KV1A_HUMAN	P01593 homo sapien
11	445	78.3	108	1	KV5O_MOUSE	P01648 mus musculu
12	445	78.3	108	2	Q9UL77	Q9ul77 homo sapien
13	443	78.0	108	1	KV5N_MOUSE	P01647 mus musculu
14	439	77.3	236	2	Q6GMW1	Q6gmw1 homo sapien
15	438	77.1	108	1	KV1P_HUMAN	P01608 homo sapien
16	436	76.8	108	1	KV1Y_HUMAN	P80362 homo sapien
17	434	76.4	108	2	Q9UL70	Q9ul70 homo sapien
18	433.5	76.3	107	2	Q96SA9	Q96sa9 homo sapien
19	433	76.2	108	1	KV1R_HUMAN	P01610 homo sapien
20	433	76.2	234	2	Q91WF8	Q91wf8 mus musculu
21	433	76.2	236	2	Q6GMX9	Q6gmx9 homo sapien
22	430	75.7	108	1	KV5U_MOUSE	P04946 mus musculu
23	430	75.7	236	2	Q7Z3Y4	Q7z3y4 homo sapien
24	429	75.5	107	2	Q9JL84	Q9jl84 mus musculu
25	429	75.5	108	1	KV1M_HUMAN	P01605 homo sapien
26	427	75.2	236	2	Q6GMX8	Q6gmx8 homo sapien
27	425	74.8	103	2	AAR11052	Aar11052 mus muscu
28	424	74.6	108	1	KV1H_HUMAN	P01600 homo sapien
29	423	74.5	236	2	Q6GMX0	Q6gmx0 homo sapien
30	422	74.3	129	1	KV1W_HUMAN	P04431 homo sapien
31	420	73.9	108	1	KV1K_HUMAN	P01603 homo sapien
32	420	73.9	108	1	KV1Q_HUMAN	P01609 homo sapien
33	419	73.8	108	1	KV1V_HUMAN	P04430 homo sapien
34	418	73.6	108	1	KV1L_HUMAN	P01604 homo sapien
35	417	73.4	108	1	KV1C_HUMAN	P01595 homo sapien
36	416.5	73.3	107	2	Q9UL81	Q9ul81 homo sapien
37	416	73.2	108	1	KV1N_HUMAN	P01606 homo sapien
38	416	73.2	116	2	Q96PF6	Q96pf6 homo sapien
39	414	72.9	236	2	Q6PIH7	Q6pih7 homo sapien
40	414	72.9	236	2	AAH34141	Aah34141 homo sapi
41	413	72.7	108	1	KV1S_HUMAN	P01611 homo sapien
42	412	72.5	108	1	KV1G_HUMAN	P01599 homo sapien
43	411	72.4	108	1	KV1E_HUMAN	P01597 homo sapien
44	411	72.4	234	2	Q7Z473	Q7z473 homo sapien
45	408.5	71.9	107	1	KV1D_HUMAN	P01596 homo sapien

ALIGNMENTS

RESULT 1
KV1B_HUMAN
ID KV1B_HUMAN STANDARD; PRT; 108 AA.
AC P01594;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain V-I region AU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72189444; PubMed=5028201;
RA Schiechl H., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
RT protein Au).";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN [2]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=77022433; PubMed=1234024;
RA Fehlhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RA Schwager P., Steigemann W., Schramm H.J.;
RT "The structure determination of the variable portion of the Bence-
RT Jones protein Au.";
RL Biophys. Struct. Mech. 1:139-146(1975).
CC -!- MISCELLANEOUS: The structure of the V region was determined by
CC molecular replacement methods using the known structure of the V
CC region of the kappa chain REI.
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A91653; K1HUAU.
DR PDB; 1JV5; X-ray; A=1-107.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT STRAND 4 5

```
FT   STRAND       10     13
FT   TURN         15     16
FT   STRAND       19     25
FT   TURN         30     31
FT   STRAND       33     38
FT   TURN         40     41
FT   STRAND       44     49
FT   TURN         50     52
FT   STRAND       53     54
FT   TURN         56     57
FT   TURN         60     61
FT   STRAND       62     67
FT   TURN         68     69
FT   STRAND       70     75
FT   HELIX        80     82
FT   STRAND       85     90
FT   STRAND       97     98
FT   STRAND      102    106
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11939 MW;  E8011187EE6F6FB9 CRC64;

  Query Match             84.5%;  Score 480;  DB 1;  Length 108;
  Best Local Similarity   85.2%;  Pred. No. 9.5e-43;
  Matches   92;  Conservative    5;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              |||||||||||||||||||||||| ||||||:||||||||| || ||||: :||| |||||
Db          1 DIQMTQSPSSLSASVGDRVTITCQASQDISDYLNWYQQKPGKAPKLLIYDASNLESGVPS 60

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              ||||||||  :| |||||||||||||:| ||  ||||||||||||||
Db         61 RFSGGGSGAHFTFTISSLQPEDIATYYCQQYDYLPWTFGQGTKVEIKR 108


RESULT 2
Q91WS9
ID   Q91WS9      PRELIMINARY;      PRT;   233 AA.
AC   Q91WS9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Colon;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Colon;
RA   Strausberg R.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC013496; AAH13496.1; -.
DR   PIR; A38740; A38740.
DR   PIR; C38740; C38740.
DR   PIR; E38740; E38740.
DR   PIR; G38740; G38740.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
FT   NON_TER       1      1
SQ   SEQUENCE   233 AA;  25781 MW;  B1C184DA149A16EB CRC64;

  Query Match             81.9%;  Score 465;  DB 2;  Length 233;
  Best Local Similarity   79.6%;  Pred. No. 9.2e-41;
  Matches   86;  Conservative   12;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              ||||||: |||||:||||||:|| || |:|||||||||  |||||:|:|:|||||||
Db         20 DIQMTQTTSSLSASLGDRVTISCSGSQGIANYLNWYQQKPDGTVKLLIYYTSSLHSGVPS 79

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              |||| ||||||:||||:|:||||||:| ||  |||||| |||:||||
Db         80 RFSGSGSGTDYSLTISNLEPEDIATYYCQQYRYLPWTFGGGTKLEIKR 127


RESULT 3
KV5J_MOUSE
ID   KV5J_MOUSE     STANDARD;      PRT;   108 AA.
AC   P01643;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig kappa chain V-V region MOPC 173.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=76091934; PubMed=812696;
RA   Schiff C., Fougereau M.;
RT   "Determination of the primary structure of a mouse IgG2a
RT   immunoglobulin. Amino-acid sequence of the light chain.";
RL   Eur. J. Biochem. 59:525-537(1975).
CC   -!- MISCELLANEOUS: This chain was isolated from a myeloma protein.
DR   PIR; A01926; KVMS73.
DR   HSSP; P01594; 1JV5.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region.
FT   DOMAIN        1     23       Framework-1.
FT   DOMAIN       24     34       Complementarity-determining-1.
FT   DOMAIN       35     49       Framework-2.
FT   DOMAIN       50     56       Complementarity-determining-2.
FT   DOMAIN       57     88       Framework-3.
FT   DOMAIN       89     97       Complementarity-determining-3.
FT   DOMAIN       98    108       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11819 MW;  2AD29D92A72AA0A3 CRC64;

  Query Match             81.2%;  Score 461;  DB 1;  Length 108;
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  Best Local Similarity   78.7%;  Pred. No. 9.6e-41;
  Matches   85;  Conservative   13;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              ||||||: |||||:|||||:|||||  | |||:|||||||  |||||:|:|:|||||||
Db          1 DIQMTQTTSSLSASLGDRVTISCSASQSIGNYLBWYQQKPDGTVKLLIYYTSSLHSGVPS 60

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              |||| ||||||:|||| |:|::||||:| |||||| ||| |||:|||| 
Db         61 RFSGSGSGTDYSLTISBLZPZBIATYYCQQYSKLPRTFGGGTKLEIKR 108


RESULT 4
Q8R062
ID   Q8R062      PRELIMINARY;      PRT;   234 AA.
AC   Q8R062;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Colon;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Colon;
RA   Strausberg R.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC027418; AAH27418.1; -.
DR   HSSP; P01594; 1JV5.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   234 AA;  25858 MW;  4EB08C81426AEAB1 CRC64;

  Query Match             81.2%;  Score 461;  DB 2;  Length 234;
  Best Local Similarity   79.6%;  Pred. No. 2.4e-40;
  Matches   86;  Conservative   13;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              ||||||: |||||:|||||:||||| |||||||||||||  |||||:|:|:|||||||
Db          1 DIQMTQTTSSLSASLGDRVTISCSASQGISNYLNWYQQKPDGTVKLLIYYTSSLHSGVPS 60

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              |||| |||| |:||||:|:|||||||:| |||: |:||| |||:|||| 
Db         81 RFSGSGSGTHYSLTISNLEPEDIATYYCQQYSQFPPTFGSGTKLEIKR 128


RESULT 5
KV1O_HUMAN
ID   KV1O_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01607;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Ig kappa chain V-I region Rei.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=76023758; PubMed=809329;
RA   Palm W., Hilschmann N.;
RT   "The primary structure of a crystalline monoclonal immunoglobulin
RT   kappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation
RT   and characterization of the tryptic peptides; the complete amino acid
RT   sequence of the protein; a contribution to the elucidation of the
RT   three-dimensional structure of antibodies, in particular their
RT   combining site.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX   MEDLINE=76039968; PubMed=1182131;
RA   Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
RT   "The molecular structure of a dimer composed of the variable portions
RT   of the Bence-Jones protein REI refined at 2.0-A resolution.";
RL   Biochemistry 14:4943-4952(1975).
CC   -!- MISCELLANEOUS: The C region of this chain has the INV (1,2)
CC       marker.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR   PIR; A91663; K1HURE.
DR   PDB; 1AR2; X-ray; @=1-107.
DR   PDB; 1BWW; X-ray; A/B=1-107.
DR   PDB; 1REI; X-ray; A/B=1-107.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Bence-Jones protein; Direct protein sequencing;
KW   Immunoglobulin V region.
FT   DOMAIN        1     23       Framework-1.
FT   DOMAIN       24     34       Complementarity-determining-1.
FT   DOMAIN       35     49       Framework-2.
FT   DOMAIN       50     56       Complementarity-determining-2.
FT   DOMAIN       57     88       Framework-3.
FT   DOMAIN       89     97       Complementarity-determining-3.
FT   DOMAIN       98    107       Framework-4.
FT   DISULFID     23     88
FT   STRAND        4      7
FT   STRAND       10     13
FT   TURN         15     16
FT   STRAND       19     25
FT   TURN         30     31
FT   STRAND       33     38
FT   TURN         40     41
FT   STRAND       45     49
FT   TURN         50     52
FT   STRAND       53     54
FT   TURN         56     57
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FT   TURN          60     61
FT   STRAND        62     67
FT   TURN          68     69
FT   STRAND        70     75
FT   HELIX         80     82
FT   STRAND        84     90
FT   STRAND        97     98
FT   STRAND       102    106
FT   NON_TER      108    108
SQ   SEQUENCE   108 AA;  11902 MW;  9E8143E1188BCE2A CRC64;

  Query Match             80.3%;  Score 456;  DB 1;  Length 108;
  Best Local Similarity   80.6%;  Pred. No. 3.2e-40;
  Matches   87;  Conservative    7;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              |||||||||||||||||||||||| |||||  ||||||| | || |||| : ||| :||||
Db          1 DIQMTQSPSSLSASVGDRVTITCQASQDIIKYLNWYQQTPGKAPKLLIYEASNLQAGVPS 60

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              |||| ||||||| |||||||||||||:| ||  ||:|||||||::| |
Db         61 RFSGSGSGTDYTFTISSLQPEDIATYYCQQYQSLPYTFGQGTKLQITR 108


RESULT 6
AAR10992
ID   AAR10992    PRELIMINARY;      PRT;   111 AA.
AC   AAR10992;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   ANA immunoglobulin kappa light chain (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=B6.Sle1; TISSUE=Spleen;
RA   Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RT   "Antinuclear autoantibodies from B6.Sle1 mice.";
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY436832; AAR10992.1; -.
FT   NON_TER       1      1
FT   NON_TER     111    111
SQ   SEQUENCE   111 AA;  12120 MW;  879A9D6B5880C59D CRC64;

  Query Match             79.9%;  Score 454;  DB 2;  Length 111;
  Best Local Similarity   81.0%;  Pred. No. 5.5e-40;
  Matches   85;  Conservative   10;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          4 MTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPSRFS 63
              |||:|||||||:||||||:| |||||||||||||||||  |||||:|:| ||||||||||
Db          1 MTQTPSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPSRFS 60

Qy         64 GGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              | |||||:||||:|: |||||||| | : |||||| |||:||||
Db         61 GSGSGTDYSLTISNLEQEDIATYFCQQGNTLPWTFGGGTKLEIKR 105


RESULT 7
KV5K_MOUSE
ID   KV5K_MOUSE     STANDARD;      PRT;   108 AA.
AC   P01644;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig kappa chain V-V region HP R16.7.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=A/J;
RX   MEDLINE=82150934; PubMed=6801658;
RA   Siegelman M., Capra J.D.;
RT   "Complete amino acid sequence of light chain variable regions derived
RT   from five monoclonal anti-p-azophenylarsonate antibodies differing
RT   with respect to a crossreactive idiotype.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC   -!- MISCELLANEOUS: Anti-arsonate hybridoma protein.
DR   PIR; A01927; KVMSAR.
DR   HSSP; P01594; 1JV5.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region.
FT   DOMAIN        1     23       Framework-1.
FT   DOMAIN       24     34       Complementarity-determining-1.
FT   DOMAIN       35     49       Framework-2.
FT   DOMAIN       50     56       Complementarity-determining-2.
FT   DOMAIN       57     88       Framework-3.
FT   DOMAIN       89     97       Complementarity-determining-3.
FT   DOMAIN       98    108       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11910 MW;  A554642C63EFF597 CRC64;

  Query Match             78.9%;  Score 448;  DB 1;  Length 108;
  Best Local Similarity   79.6%;  Pred. No. 2.3e-39;
  Matches   86;  Conservative   10;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              ||||||: ||||||:||||||:| |||||||||||||||  |||||:|:| |||||||
Db          1 DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 60

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              |||| ||||||:||||:|: |||||||| | : || ||| |||:||||
Db         61 RFSGSGSGTDYSLTISNLEQEDIATYFCQQGNSLPRTFGGGTKLEIKR 108


RESULT 8
KV5L_MOUSE
ID   KV5L_MOUSE     STANDARD;      PRT;   108 AA.
AC   P01645;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig kappa chain V-V region HP 93G7.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=A/J;
RX   MEDLINE=82150934; PubMed=6801658;
RA   Siegelman M., Capra J.D.;
RT   "Complete amino acid sequence of light chain variable regions derived
RT   from five monoclonal anti-p-azophenylarsonate antibodies differing
RT   with respect to a crossreactive idiotype.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC   -!- MISCELLANEOUS: Anti-arsonate hybridoma protein.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region.
FT   DOMAIN        1     23       Framework-1.
FT   DOMAIN       24     34       Complementarity-determining-1.
FT   DOMAIN       35     49       Framework-2.
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FT   DOMAIN       50     56       Complementarity-determining-2.
FT   DOMAIN       57     88       Framework-3.
FT   DOMAIN       89     97       Complementarity-determining-3.
FT   DOMAIN       98    108       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11954 MW;  22F4642C63EFF58E CRC64;

  Query Match             78.7%;  Score 447;  DB 1;  Length 108;
  Best Local Similarity   79.6%;  Pred. No. 2.9e-39;
  Matches   86;  Conservative   10;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              |||||| |||||:|||||:| ||||||||||||||||  |||||:|:| |||||||
Db          1 DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 60

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              |||| ||||||:||||:|: |||||||| | : || ||| |||:||||
Db         61 RFSGSGSGTDYSLTISNLEQEDIATYFCQQGNMLPRTFGGGTKLEIKR 108


RESULT 9
KV5M_MOUSE
ID   KV5M_MOUSE     STANDARD;      PRT;   108 AA.
AC   P01646;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig kappa chain V-V region HP 123E6.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=A/J;
RX   MEDLINE=82150934; PubMed=6801658;
RA   Siegelman M., Capra J.D.;
RT   "Complete amino acid sequence of light chain variable regions derived
RT   from five monoclonal anti-p-azophenylarsonate antibodies differing
RT   with respect to a crossreactive idiotype.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC   -!- MISCELLANEOUS: Anti-arsonate hybridoma protein.
DR   HSSP; P01594; 1JV5.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region.
FT   DOMAIN        1     23       Framework-1.
FT   DOMAIN       24     34       Complementarity-determining-1.
FT   DOMAIN       35     49       Framework-2.
FT   DOMAIN       50     56       Complementarity-determining-2.
FT   DOMAIN       57     88       Framework-3.
FT   DOMAIN       89     97       Complementarity-determining-3.
FT   DOMAIN       98    108       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11989 MW;  4C98599C08EBA09A CRC64;

  Query Match             78.7%;  Score 447;  DB 1;  Length 108;
  Best Local Similarity   80.6%;  Pred. No. 2.9e-39;
  Matches   87;  Conservative    8;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              ||||||| |||||:||||||:| ||||||||||||||||  |||||:|:| |||||||
Db          1 DIQMTQSTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 60

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              |||| ||||||:||||:|: |||||||| |   || ||| |||:||||
Db         61 RFSGSGSGTDYSLTISNLEQEDIATYFCQQGYMLPRTFGGGTKLEIKR 108


RESULT 10
KV1A_HUMAN
ID   KV1A_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01593;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig kappa chain V-I region AG.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=69234734; PubMed=4893682;
RA   Titani K., Shinoda T., Putnam F.W.;
RT   "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT   complete sequence and the location of the disulfide bridges.";
RL   J. Biol. Chem. 244:3550-3560(1969).
CC   -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR   PIR; A01861; K1HUAG.
DR   HSSP; P01607; 1BWW.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Bence-Jones protein; Direct protein sequencing;
KW   Immunoglobulin V region.
FT   DOMAIN        1     23       Framework-1.
FT   DOMAIN       24     34       Complementarity-determining-1.
FT   DOMAIN       35     49       Framework-2.
FT   DOMAIN       50     56       Complementarity-determining-2.
FT   DOMAIN       57     88       Framework-3.
FT   DOMAIN       89     97       Complementarity-determining-3.
FT   DOMAIN       98    107       Framework-4.
FT   DISULFID     23     88
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11992 MW;  E3B3B246C18F0C4F CRC64;

  Query Match             78.3%;  Score 445;  DB 1;  Length 108;
  Best Local Similarity   78.7%;  Pred. No. 4.7e-39;
  Matches   85;  Conservative    9;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              |||||||||||||||||||||||| |||||::|||||| | || |:||: :||| :||||
Db          1 DIQMTQSPSSLSASVGDRVTITCQASQDINHYLNWYQQGPKKAPKILIYDASNLETGVPS 60

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              |||| | |||:| ||| |||||||||:| ||  || |||||||:||||
Db         61 RFSGSGFGTDFTFTISGLQPEDIATYYCQQYDTLPRTFGQGTKLEIKR 108


RESULT 11
KV5O_MOUSE
ID   KV5O_MOUSE     STANDARD;      PRT;   108 AA.
AC   P01648;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig kappa chain V-V region HP 91A3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=A/J;
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RX   MEDLINE=82150934; PubMed=6801658;
RA   Siegelman M., Capra J.D.;
RT   "Complete amino acid sequence of light chain variable regions derived
RT   from five monoclonal anti-p-azophenylarsonate antibodies differing
RT   with respect to a crossreactive idiotype.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC   -!- MISCELLANEOUS: Anti-arsonate hybridoma protein.
DR   HSSP; P01594; 1JV5.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region.
FT   DOMAIN        1     23       Framework-1.
FT   DOMAIN       24     34       Complementarity-determining-1.
FT   DOMAIN       35     49       Framework-2.
FT   DOMAIN       50     56       Complementarity-determining-2.
FT   DOMAIN       57     88       Framework-3.
FT   DOMAIN       89     97       Complementarity-determining-3.
FT   DOMAIN       98    108       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11961 MW;  D52EDA5E9A45291C CRC64;

  Query Match             78.3%;  Score 445;  DB 1;  Length 108;
  Best Local Similarity   77.8%;  Pred. No. 4.7e-39;
  Matches   84;  Conservative   13;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              ||||||:|||||||:||||||:| |||||:||||||:|||| |||||:|:| |||||||
Db          1 DIQMTQTPSSLSASLGDRVTISCRASQDINNYLNWYRQKPDGTVKLLIYYTSRLHSGVPS 60

Qy         61 RFSGGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              |||| ||||||:||||:|: |||:|||| | : || ||| |||:||||
Db         61 RFSGSGSGTDYSLTISNLEQEDISTYFCQQGNALPRTFGGGTKLEIKR 108


RESULT 12
Q9UL77
ID   Q9UL77      PRELIMINARY;      PRT;   108 AA.
AC   Q9UL77;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035037; AAD56273.1; -.
DR   PIR; B49047; B49047.
DR   PIR; S34083; S34083.
DR   HSSP; P01607; 1BWW.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11738 MW;  C06681716C4D16F3 CRC64;

  Query Match             78.3%;  Score 445;  DB 2;  Length 108;
  Best Local Similarity   79.6%;  Pred. No. 4.7e-39;
  Matches   86;  Conservative    7;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              ||||||||||||||||||||||| ||| ||:||||||||| ||  |||: :|:| |||||
Db          1 DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPNLLIYAASSLQSGVPS 60

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              |||| |||||:|||||||||||| |||:| |    ||||:||||||||
Db         61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTSWTFGEGTKVEIKR 108


RESULT 13
KV5N_MOUSE
ID   KV5N_MOUSE     STANDARD;      PRT;   108 AA.
AC   P01647;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig kappa chain V-V region HP 124E1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=A/J;
RX   MEDLINE=82150934; PubMed=6801658;
RA   Siegelman M., Capra J.D.;
RT   "Complete amino acid sequence of light chain variable regions derived
RT   from five monoclonal anti-p-azophenylarsonate antibodies differing
RT   with respect to a crossreactive idiotype.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC   -!- MISCELLANEOUS: Anti-arsonate hybridoma protein.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region.
FT   DOMAIN        1     23       Framework-1.
FT   DOMAIN       24     34       Complementarity-determining-1.
FT   DOMAIN       35     49       Framework-2.
FT   DOMAIN       50     56       Complementarity-determining-2.
FT   DOMAIN       57     88       Framework-3.
FT   DOMAIN       89     97       Complementarity-determining-3.
FT   DOMAIN       98    108       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11965 MW;  39971BC653EFEFA2 CRC64;

  Query Match             78.0%;  Score 443;  DB 1;  Length 108;
  Best Local Similarity   78.7%;  Pred. No. 7.7e-39;
  Matches   85;  Conservative   10;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              ||||||: ||||||:||||||:| |||||:||||||||||  |||||:|:| |||||||
Db          1 DIQMTQTTSSLSASLGDRVTISCRASQDINNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 60

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              |||| ||||||:||||:|: ||||||| |    || ||| |||:||||
Db         61 RFSGSGSGTDYSLTISNLEQEDIATYFCQQGKTLPRTFGGGTKLEIKR 108


RESULT 14
Q6GMW1
ID   Q6GMW1      PRELIMINARY;      PRT;   236 AA.
AC   Q6GMW1;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
```

```
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073791; AAH73791.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25751 MW;  5BFE6A087AFAC437 CRC64;

  Query Match             77.3%;  Score 439;  DB 2;  Length 236;
  Best Local Similarity   81.3%;  Pred. No. 5.2e-38;
  Matches   87;  Conservative    5;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          2 IQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPSR 61
              |||||||||||||||||||||| ||| ||| | |||||| || ||||: :|:| ||||||
Db         24 IQMTQSPSSLSASVGDRVTITCRASQGISNDLGWYQQKPGKAPKLLIYAASSLQSGVPSR 83

Qy         62 FSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              ||| |||||:|||||||||||| |||:| |    ||||||||||||||
Db         84 FSGSGSGTDFTLTISSLQPEDFATYYCLQDYNYPWTFGQGTKVEIKR 130


RESULT 15
KV1P_HUMAN
ID   KV1P_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01608;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig kappa chain V-I region Roy.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=68362076; PubMed=5595110;
RA   Hilschmann N.;
RT   "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
RT   Cum.).";
RL   Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
RN   [2]
RP   REVISIONS TO 39 AND 41.
RA   Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
RA   Steinmetz-Kayne M., Suter L., Watanabe S.;
RL   (In) Franek F., Shugar D. (eds.);
RL   Gamma globulins: structure and function, pp.57-74, Academic Press, New
RL   York (1969).
CC   -!- MISCELLANEOUS: The C region of this chain has the INV (1,2)
CC       marker.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR   PIR; A91638; K1HURY.
DR   HSSP; P01607; 1BWW.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Bence-Jones protein; Direct protein sequencing;
KW   Immunoglobulin V region.
FT   DOMAIN        1     23       Framework-1.
FT   DOMAIN       24     34       Complementarity-determining-1.
FT   DOMAIN       35     49       Framework-2.
FT   DOMAIN       50     56       Complementarity-determining-2.
FT   DOMAIN       57     88       Framework-3.
FT   DOMAIN       89     97       Complementarity-determining-3.
FT   DOMAIN       98    107       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11782 MW;  F5ACEDE5A313DF3A CRC64;

  Query Match             77.1%;  Score 438;  DB 1;  Length 108;
  Best Local Similarity   78.7%;  Pred. No. 2.6e-38;
  Matches   85;  Conservative    8;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPDKAVKLLIFYSSNLHSGVPS 60
              |||||||||||||||||||||| |||||| :|||||||| || ||||: :| | :||||
Db          1 DIQMTQSPSSLSASVGDRVTITCQASQDISIFLNWYQQKPGKAPKLLIYDASKLEAGVPS 60

Qy         61 RFSGGGSGTDYTLTISSLQPEDIATYFCHQYSKLPWTFGQGTKVEIKR 108
              |||| |||||:| |||||||||||||:| |:  || ||| ||||: ||
Db         61 RFSGTGSGTDFTFTISSLQPEDIATYYCQQFDNLPLTFGGGTKVDFKR 108


Search completed: December 23, 2004, 19:04:38
Job time : 31.044 secs
```

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2004, 18:30:04 ; Search time 31.8339 Seconds
(without alignments)
1340.986 Million cell updates/sec

Title: US-10-089-500-55
Perfect score: 624
Sequence: 1 EVTLVESGGDFVKPGGSLKV.....KLGTYYFDSWGQGTTLTVSS 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	624	100.0	119	4	AAB81989	Aab81989 Gangliosi
2	624	100.0	119	6	ABU11012	Abu11012 Modified
3	624	100.0	130	2	AAR33256	Aar33256 Rat immun
4	624	100.0	130	2	AAR53341	Aar53341 KM641 L c
5	624	100.0	130	2	AAY28369	Aay28369 pKM641 HA
6	624	100.0	130	3	AAB01627	Aab01627 Murine im
7	624	100.0	138	4	AAB81977	Aab81977 Gangliosi
8	624	100.0	138	6	ABU11002	Abu11002 Modified
9	624	100.0	582	4	AAB81991	Aab81991 Gangliosi
10	579	92.8	119	4	AAB81985	Aab81985 Gangliosi
11	579	92.8	119	6	ABU11010	Abu11010 Modified
12	579	92.8	582	4	AAB81987	Aab81987 Gangliosi
13	493	79.0	119	2	AAW29994	Aaw29994 Heavy cha
14	487	78.0	134	6	ABP60555	Abp60555 Murine an
15	486.5	78.0	294	4	AAB20442	Aab20442 Anti-FIX/
16	486.5	78.0	325	4	AAB20438	Aab20438 Anti-FIX/
17	486.5	78.0	732	4	AAB20437	Aab20437 Anti-FIX/
18	486	77.9	140	6	ABG74241	Abg74241 Mouse ant
19	486	77.9	247	2	AAW11917	Aaw11917 Murine MA
20	482.5	77.3	249	4	AAB20436	Aab20436 Anti-FIX/
21	481	77.1	121	5	AAE16426	Aae16426 Mouse ant
22	480.5	77.0	121	6	ABR41818	Abr41818 Heavy cha
23	480	76.9	119	2	AAW29996	Aaw29996 Humanised
24	480	76.9	237	7	AAE38657	Aae38657 Mouse G1
25	477.5	76.5	121	8	ADM78071	Adm78071 Human SKB
26	477	76.4	232	7	ADF72730	Adf72730 Divalent
27	477	76.4	241	7	ADF72729	Adf72729 Monovalen
28	477	76.4	255	7	ADF72734	Adf72734 His-tagge
29	475.5	76.2	249	4	AAB20435	Aab20435 Anti-FIX/
30	475	76.1	119	5	AAU72814	Aau72814 Humanised
31	475	76.1	119	6	AAO29882	Aao29882 M type fu
32	475	76.1	119	7	ADJ79825	Adj79825 M-type hu
33	475	76.1	249	4	AAB20434	Aab20434 Anti-FIX/
34	475	76.1	462	6	AAO29869	Aao29869 Mouse ant
35	475	76.1	462	7	ADJ79787	Adj79787 TRA-8 ant
36	475	76.1	464	5	AAU72801	Aau72801 TRA-8 hea
37	473.5	75.9	120	5	AAO18391	Aao18391 Murine CB
38	472	75.6	119	2	AAR79887	Aar79887 Anti-EGFR
39	472	75.6	239	2	AAR79866	Aar79866 Anti-EGFR
40	471	75.5	262	6	ABR42295	Abr42295 Bispecifi
41	471	75.5	262	6	ABR42293	Abr42293 Bispecifi
42	471	75.5	262	6	ABR42290	Abr42290 Diabody h
43	471	75.5	262	6	ABR42291	Abr42291 Bispecifi
44	471	75.5	268	6	ABR42288	Abr42288 Diabody 6
45	471	75.5	268	6	ABR42287	Abr42287 Diabody 6

ALIGNMENTS

RESULT 1
AAB81989
ID AAB81989 standard; protein; 119 AA.
XX
AC AAB81989;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 55.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
XX
OS Mus musculus.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Claim 10; Page 173-174; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 119 AA;

Query Match 100.0%; Score 624; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 7.4e-51;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119


RESULT 2
ABU11012
ID   ABU11012 standard; protein; 119 AA.
XX
AC   ABU11012;
XX
DT   04-FEB-2003  (first entry)
XX
DE   Modified ganglioside GD3 antibody associated protein #5.
XX
KW   Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
XX
OS   Mus musculus.
XX
PN   WO200278739-A1.
XX
PD   10-OCT-2002.
XX
PF   29-MAR-2002; 2002WO-JP003170.
XX
PR   29-MAR-2001; 2001JP-00097483.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Shitara K,  Niwa R,  Kanazawa J,  Asada M;
XX
DR   WPI; 2003-067410/06.
XX
PT   Drugs containing genetically-modified antibody against ganglioside GD3,
PT   its fragment, immunocompetent cell activators or/and antitumor agents in
PT   combination, applicable in treating malignant tumor like melanoma.
XX
PS   Claim 7; Page 112-113; 121pp; Japanese.
XX
CC   The invention describes drugs contain a genetically-modified antibody
CC   against ganglioside GD3 or its fragment and at least 1 of a substance
CC   capable of activating immunocompetent cells and a substance having an
CC   antitumor activity in combination. The drugs can be used to treat tumour
CC   like melanoma and can provide a treatment with enhanced therapeutic
CC   effect and little side-reactions, particularly to relieve problems of
CC   side-effects during the conventional single administration. This sequence
CC   represents a protein associated with the anti- ganglioside GD3 antibody
XX
SQ   Sequence 119 AA;

  Query Match             100.0%;  Score 624;  DB 6;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 7.4e-51;
  Matches  119;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119


RESULT 3
AAR33256
ID   AAR33256 standard; protein; 130 AA.
XX
AC   AAR33256;
XX
DT   25-MAR-2003  (revised)
DT   12-JUL-1993  (first entry)
XX
DE   Rat immunoglobulin H chain varible region of pKM641HA3.
XX
KW   Promoter; variable; region; rat; immunoglobulin; heavy; H; chain;
KW   humanised; chimeric; antibody; expression vector.
XX
OS   Rattus rattus.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .10
FT                   /note= "Signal peptide"
FT   Protein         11. .130
FT                   /note= "Mature protein"
XX
PN   EP533199-A2.
XX
PD   24-MAR-1993.
XX
PF   18-SEP-1992;   92EP-00116026.
XX
PR   18-SEP-1991;   91JP-00238375.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO CO LTD.
XX
PI   Shitara K,  Hanai N,  Hasegawa M,  Miyaji H,  Kuwana Y;
XX
DR   WPI; 1993-095510/12.
DR   N-PSDB; AAQ33257.
XX
PT   Humanised chimeric antibody prodn. against ganglioside GD3 - for treating
PT   cancers, such as melanoma, neuroblastoma, etc.
XX
PS   Claim 6; Page 29-30; 63pp; English.
XX
CC   The sequences given in AAR33256-57 represent rat heavy and light chain
CC   variable regions respectively. The DNA sequences encoding these proteins
CC   were used in the construction of humanised chimeric antibody expression
CC   vectors. In these humanised antibodies none of the amino acids of the non
CC   -human animal Ab variable region have been changed. (Updated on 25-MAR-
CC   2003 to correct PN field.)
XX
SQ   Sequence 130 AA;

  Query Match             100.0%;  Score 624;  DB 2;  Length 130;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-51;
  Matches  119;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         11 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 70

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 129


RESULT 4
AAR53341
ID   AAR53341 standard; protein; 130 AA.
XX
AC   AAR53341;
XX
DT   18-NOV-1994  (first entry)
XX
DE   KM641 L chain variable region.
XX
KW   Monoclonal antibody; Ab; ganglioside GM2; chimera; chimeric antibody;
KW   expression vector; heavy; light; chain; hypervariable region; CDR;
KW   constant region; hybridoma; Ig; immunoglobulin; promoter; enhancer.
XX
```

```
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .10
FT                   /label= sig_peptide
XX
PN   AU9346181-A.
XX
PD   17-MAR-1994.
XX
PF   07-SEP-1993;   93AU-00046181.
XX
PR   07-SEP-1992;   92JP-00238452.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Nakamura K,  Koike M,  Shitara K,  Hanai N,  Kuwana Y,  Hasegawa M;
XX
DR   WPI; 1994-126857/16.
DR   N-PSDB; AAQ45439.
XX
PT   Humanised antibody specific for ganglioside GM2 - used for producing a
PT   cytocidal effect on cancers such as melanoma, neuroblastoma and glioma.
XX
PS   Example 2; Page 116-117; 191pp; English.
XX
CC   Example 2 describes the construction of the vector pChi641HA1 for
CC   chimeric human antibody H chain expression. mRNA from mouse anti-GD3
CC   monoclonal Ab KM641-producing cells was isolated and KM641 H and L chain
CC   cDNAs isolated. The base sequences of the Ig variable regions in KM641 H
CC   chain cDNA (pKM641HA3) and KM641 L chain cDNA (pKM641LA2) are given in
CC   AAQ45438-39. A KM641-derived chimeric human Ab H chain expression vector
CC   was constructed by joining the H chain variable region gene from
CC   pKM641HA3 to a vector for chimeric human Ab H chain expression using the
CC   synthetic DNAs given in AAQ63439 and AAQ63440
XX
SQ   Sequence 130 AA;

  Query Match             100.0%;  Score 624;  DB 2;  Length 130;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-51;
  Matches  119;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         11 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 70

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 129


RESULT 5
AAY28369
ID   AAY28369 standard; protein; 130 AA.
XX
AC   AAY28369;
XX
DT   04-NOV-1999  (first entry)
XX
DE   pKM641 HA3 immunoglobulin heavy chain.
XX
KW   antibody; nucleotide; genomic; hypervariable region; chimeric;
KW   light chain; amino acid.
XX
OS   Mus sp.
XX
PN   US5939532-A.
XX
PD   17-AUG-1999.
XX
PF   07-JUN-1995;   95US-00483528.
XX
PR   07-SEP-1993;   93US-00116778.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Nakamura K,  Hanai N,  Kuwana Y,  Hasegawa M,  Koike M,  Shitara K;
XX
DR   WPI; 1999-468416/39.
DR   N-PSDB; AAX99482.
XX
PT   Chimeric human antibody expression vectors.
XX
PS   Example 1; Col 99-101; 188pp; English.
XX
CC   This immunoglobulin region was isolated from pKM641HA3. This sequence has
CC   no methionine initiation codon and the leader sequence was partly
CC   lacking. The chimeric human antibodies are useful in the treatment of
CC   cancer, especially that which is of neural ectodermal origin. In contrast
CC   to prior art constructs based on mouse monoclonal antibodies, the
CC   chimeric human antibodies do not cause anti-mouse immunoglobulin
CC   production. The chimeric human antibodies have a prolonged half-life and
CC   a reduced frequency of adverse effects when compared to mouse monoclonal
CC   antibodies
XX
SQ   Sequence 130 AA;

  Query Match             100.0%;  Score 624;  DB 2;  Length 130;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-51;
  Matches  119;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         11 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 70

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 129


RESULT 6
AAB01627
ID   AAB01627 standard; protein; 130 AA.
XX
AC   AAB01627;
XX
DT   07-DEC-2000  (first entry)
XX
DE   Murine immunoglobulin heavy chain variable region.
XX
KW   Mouse; immunoglobulin; H chain; heavy chain; variable region; cancer;
KW   humanised antibody.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .10
FT                   /label= signal_peptide
FT   Protein         11. .130
FT                   /label= mature_immunoglobulin_heavy_chain_variable region
XX
PN   EP1013761-A2.
XX
PD   28-JUN-2000.
XX
PF   18-SEP-1992;   99EP-00124345.
XX
PR   18-SEP-1991;   91JP-00238375.
PR   18-SEP-1992;   92EP-00116026.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Shitara K,  Hanai N,  Hasegawa M,  Miyaji H,  Kuwana Y;
XX
DR   WPI; 2000-402204/35.
DR   N-PSDB; AAA51003.
```

```
XX
PT   New humanized chimera antibody KM-871 useful for treating cancer,
PT   comprises variable region of mouse monoclonal antibody, reactive with
PT   ganglioside and human antibody constant region.
XX
PS   Claim 14; Page 27-28; 65pp; English.
XX
CC   The present sequence is a murine immunoglobulin heavy chain variable
CC   region from plasmid KM-641. The coding sequence was used in the creation
CC   of an expression vector, along with the sequence for a human antibody, to
CC   produce humanised chimaeric antibodies, which can be used to treat
CC   cancer. Humanised chimaeric antibodies are more effective than mouse
CC   antibodies as they do not provoke a reaction in the human and side
CC   effects, such as the formation of anti-mouse immunoglobulin antibody and
CC   the rapid half-life of the immunoglobulins, do not occur
XX
SQ   Sequence 130 AA;

  Query Match             100.0%;  Score 624;  DB 3;  Length 130;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-51;
  Matches  119;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         11 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 70

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 129


RESULT 7
AAB81977
ID   AAB81977 standard; protein; 138 AA.
XX
AC   AAB81977;
XX
DT   03-JUL-2001  (first entry)
XX
DE   Ganglioside GD3 specific antibody related protein SEQ ID NO: 1.
XX
KW   Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW   cancer.
XX
OS   Mus musculus.
XX
PN   WO200123432-A1.
XX
PD   05-APR-2001.
XX
PF   29-SEP-2000; 2000WO-JP006774.
XX
PR   30-SEP-1999;   99JP-00278291.
PR   06-APR-2000; 2000JP-00105088.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Hanai N,  Shitara K,  Nakamura K,  Niwa R;
XX
DR   WPI; 2001-266143/27.
XX
PT   New human type complementation-determining region-transplanted antibody
PT   and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT   of e.g. tumors, with low antigenicity, little side effects but potent
PT   activity in cancer.
XX
PS   Example 1; Page 138-139; 183pp; Japanese.
XX
CC   The present invention describes a monoclonal antibody which can react
CC   specifically with ganglioside GD3. The antibody and its derivatives are
CC   useful in the diagnosis and therapy of tumours, particularly cancer
CC   diagnosis. The present sequence is a protein used in the exemplification
CC   of the invention
XX
SQ   Sequence 138 AA;

  Query Match             100.0%;  Score 624;  DB 4;  Length 138;
  Best Local Similarity   100.0%;  Pred. No. 8.7e-51;
  Matches  119;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         20 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 79

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 138


RESULT 8
ABU11002
ID   ABU11002 standard; protein; 138 AA.
XX
AC   ABU11002;
XX
DT   04-FEB-2003  (first entry)
XX
DE   Modified ganglioside GD3 antibody associated protein #1.
XX
KW   Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
XX
OS   Mus musculus.
XX
PN   WO200278739-A1.
XX
PD   10-OCT-2002.
XX
PF   29-MAR-2002; 2002WO-JP003170.
XX
PR   29-MAR-2001; 2001JP-00097483.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Shitara K,  Niwa R,  Kanazawa J,  Asada M;
XX
DR   WPI; 2003-067410/06.
XX
PT   Drugs containing genetically-modified antibody against ganglioside GD3,
PT   its fragment, immunocompetent cell activators or/and antitumor agents in
PT   combination, applicable in treating malignant tumor like melanoma.
XX
PS   Example 3; Page 97; 121pp; Japanese.
XX
CC   The invention describes drugs contain a genetically-modified antibody
CC   against ganglioside GD3 or its fragment and at least 1 of a substance
CC   capable of activating immunocompetent cells and a substance having an
CC   antitumor activity in combination. The drugs can be used to treat tumour
CC   like melanoma and can provide a treatment with enhanced therapeutic
CC   effect and little side-reactions, particularly to relieve problems of
CC   side-effects during the conventional single administration. This sequence
CC   represents a protein associated with the anti- ganglioside GD3 antibody
XX
SQ   Sequence 138 AA;

  Query Match             100.0%;  Score 624;  DB 6;  Length 138;
  Best Local Similarity   100.0%;  Pred. No. 8.7e-51;
  Matches  119;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         20 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 79

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 138
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RESULT 9
AAB81991
ID   AAB81991 standard; protein; 582 AA.
XX
AC   AAB81991;
XX
DT   03-JUL-2001  (first entry)
XX
DE   Ganglioside GD3 specific antibody related protein SEQ ID NO: 57.
XX
KW   Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW   cancer.
XX
OS   Synthetic.
XX
PN   WO200123432-A1.
XX
PD   05-APR-2001.
XX
PF   29-SEP-2000; 2000WO-JP006774.
XX
PR   30-SEP-1999;   99JP-00278291.
PR   06-APR-2000; 2000JP-00105088.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Hanai N,  Shitara K,  Nakamura K,  Niwa R;
XX
DR   WPI; 2001-266143/27.
XX
PT   New human type complementation-determining region-transplanted antibody
PT   and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT   of e.g. tumors, with low antigenicity, little side effects but potent
PT   activity in cancer.
XX
PS   Claim 39; Page 175-179; 183pp; Japanese.
XX
CC   The present invention describes a monoclonal antibody which can react
CC   specifically with ganglioside GD3. The antibody and its derivatives are
CC   useful in the diagnosis and therapy of tumours, particularly cancer
CC   diagnosis. The present sequence is a protein used in the exemplification
CC   of the invention
XX
SQ   Sequence 582 AA;

  Query Match             100.0%;  Score 624;  DB 4;  Length 582;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-50;
  Matches  119;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119


RESULT 10
AAB81985
ID   AAB81985 standard; protein; 119 AA.
XX
AC   AAB81985;
XX
DT   03-JUL-2001  (first entry)
XX
DE   Ganglioside GD3 specific antibody related protein SEQ ID NO: 9.
XX
KW   Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW   cancer.
XX
OS   Synthetic.
XX
PN   WO200123432-A1.
XX
PD   05-APR-2001.
XX
PF   29-SEP-2000; 2000WO-JP006774.
XX
PR   30-SEP-1999;   99JP-00278291.
PR   06-APR-2000; 2000JP-00105088.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Hanai N,  Shitara K,  Nakamura K,  Niwa R;
XX
DR   WPI; 2001-266143/27.
XX
PT   New human type complementation-determining region-transplanted antibody
PT   and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT   of e.g. tumors, with low antigenicity, little side effects but potent
PT   activity in cancer.
XX
PS   Claim 20; Page 142-143; 183pp; Japanese.
XX
CC   The present invention describes a monoclonal antibody which can react
CC   specifically with ganglioside GD3. The antibody and its derivatives are
CC   useful in the diagnosis and therapy of tumours, particularly cancer
CC   diagnosis. The present sequence is a protein used in the exemplification
CC   of the invention
XX
SQ   Sequence 119 AA;

  Query Match             92.8%;  Score 579;  DB 4;  Length 119;
  Best Local Similarity   91.6%;  Pred. No. 1.2e-46;
  Matches  109;  Conservative    5;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || |||||||||:|||||:||||||||||||||||||| | | ||||||||||||||||
Db          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
              |||||||||||||:|||||||||||:|||||:|||||||||||||||||| |||||
Db         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYFDSWGQGTLLTVSS 119


RESULT 11
ABU11010
ID   ABU11010 standard; protein; 119 AA.
XX
AC   ABU11010;
XX
DT   04-FEB-2003  (first entry)
XX
DE   Modified ganglioside GD3 antibody associated protein #3.
XX
KW   Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
XX
OS   Synthetic.
XX
PN   WO200278739-A1.
XX
PD   10-OCT-2002.
XX
PF   29-MAR-2002; 2002WO-JP003170.
XX
PR   29-MAR-2001; 2001JP-00097483.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Shitara K,  Niwa R,  Kanazawa J,  Asada M;
XX
DR   WPI; 2003-067410/06.
XX
PT   Drugs containing genetically-modified antibody against ganglioside GD3,
```

PT its fragment, immunocompetent cell activators or/and antitumor agents in
PT combination, applicable in treating malignant tumor like melanoma.
XX
PS Claim 8; Page 99; 121pp; Japanese.
XX
CC The invention describes drugs contain a genetically-modified antibody
CC against ganglioside GD3 or its fragment and at least 1 of a substance
CC capable of activating immunocompetent cells and a substance having an
CC antitumor activity in combination. The drugs can be used to treat tumour
CC like melanoma and can provide a treatment with enhanced therapeutic
CC effect and little side-reactions, particularly to relieve problems of
CC side-effects during the conventional single administration. This sequence
CC represents a protein associated with the anti- ganglioside GD3 antibody
XX
SQ Sequence 119 AA;

Query Match 92.8%; Score 579; DB 6; Length 119;
Best Local Similarity 91.6%; Pred. No. 1.2e-46;
Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
|| |||||||||:|||||:||||||||||||||||||| | | ||||||||||||||||
Db 1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60

Qy 61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
||||||||||||||:||||||||||:||||:||||||||||||||||||| |||||
Db 61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYFDSWGQGTLLTVSS 119

RESULT 12
AAB81987
ID AAB81987 standard; protein; 582 AA.
XX
AC AAB81987;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 53.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Claim 41; Page 168-172; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 582 AA;

Query Match 92.8%; Score 579; DB 4; Length 582;
Best Local Similarity 91.6%; Pred. No. 7e-46;
Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
|| |||||||||:|||||:||||||||||||||||||| | | ||||||||||||||||
Db 1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60

Qy 61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
||||||||||||||:||||||||||:||||:||||||||||||||||||| |||||
Db 61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYFDSWGQGTLLTVSS 119

RESULT 13
AAW29994
ID AAW29994 standard; protein; 119 AA.
XX
AC AAW29994;
XX
DT 25-MAR-2003 (revised)
DT 12-MAR-1998 (first entry)
XX
DE Heavy chain variable region of MAb ior t1A.
XX
KW Heavy chain; variable region; monoclonal antibody; human; CD6; murine;
KW leukocyte differentiation antigen; hybridoma; humanisation; mutagenesis;
KW PCR; primer; amplification; inflammatory infiltration; skin; psoriasis;
KW diagnosis.
XX
OS Mus sp.
XX
PN WO9719111-A2.
XX
PD 29-MAY-1997.
XX
PF 18-NOV-1996; 96WO-CU000004.
XX
PR 17-NOV-1995; 95CU-00000120.
XX
PA (IMMU-) CENT IMMUNOLOGIA MOLECULAR.
XX
PI Montero Casimiro JE, Lombardero Valladares J, Perez Rodriguez R;
PI Sierra Blazquez P, Tormo Bravo BR;
XX
DR WPI; 1997-298060/27.
XX
PT Monoclonal antibody against human CD6 antigen - useful for diagnosis and
PT treatment of psoriasis.
XX
PS Claim 3; Page 27; 38pp; Spanish.
XX
CC This is the amino acid sequence of the heavy chain variable region of the
CC monoclonal antibody (MAb) ior T1A which recognises the human leukocyte
CC differentiation antigen CD6. The MAb is a murine IgG2-type Ab produced by
CC the usual hybridoma techniques. The coding sequence for the variable
CC region can be used to generate humanised variants, especially by
CC mutagenic PCR. CD6 has been shown to be expressed in T lymphocytes
CC involved in the inflammatory infiltration of the skin in psoriasis. The
CC anti-CD6 MAb can therefore be used to diagnose and treat psoriasis.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 119 AA;

Query Match 79.0%; Score 493; DB 2; Length 119;
Best Local Similarity 81.5%; Pred. No. 1.5e-38;
Matches 97; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

Qy 1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
|| |||||| |||||||:||||||| || |||||||||| ||||||| |||||| ||
Db 1 EVQLVESGGGLVKPGGSLKLSCAASGFKFSRYAMSWVRQTPEKRLEWVATISSGGSYIYY 60

Qy 61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119

```
                  |||||||||||||| |||||||| ||||||:|||:| |      ||||||||||||||||
Db          61 PDSVKGRFTISRDNVKNTLYLQMSSLRSEDTAMYYCARRDYDLDYFDSWGQGTTLTVSS 119

RESULT 14
ABP60555
ID   ABP60555 standard; protein; 134 AA.
XX
AC   ABP60555;
XX
DT   21-MAR-2003  (first entry)
XX
DE   Murine antibody 14F3 heavy chain variable region.
XX
KW   Mouse; monoclonal antibody; 14F3; osteopathic; antirheumatic;
KW   antiarthritic; antiinflammatory; cytostatic; antipsoriatic; antidiabetic;
KW   neuroprotective; gene therapy; rheumatoid arthritis; osteoporosis;
KW   bone cancer; osteolysis; osteoarthritis; immune disease; psoriasis;
KW   insulin-dependent diabetes; inflammatory bowel disease;
KW   multiple sclerosis; heavy chain variable region;
KW   complementary determining region; CDR.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Region          31. .35
FT                   /label= CDR1
FT   Region          50. .66
FT                   /label= CDR2
FT   Region          99. .110
FT                   /label= CDR3
XX
PN   WO200295012-A1.
XX
PD   28-NOV-2002.
XX
PF   03-MAY-2002; 2002WO-US014246.
XX
PR   18-MAY-2001; 2001US-0292031P.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI   Sweet RW,  Tornetta MA,  Wattam TA;
XX
DR   WPI; 2003-156758/15.
DR   N-PSDB; ABV99887.
XX
PT   New monoclonal antibody having the characteristics of a monoclonal
PT   antibody 14F3, useful for treating or preventing osteopathic diseases,
PT   e.g. rheumatoid arthritis, or osteoporosis, and immune diseases e.g.
PT   psoriasis, or diabetes.
XX
PS   Disclosure; Page 8; 51pp; English.
XX
CC   The invention relates to a novel monoclonal antibody having the
CC   identifying characteristics of, or that is a monoclonal antibody 14F3. An
CC   antibody of the invention has osteopathic, antirheumatic, antiarthritic,
CC   antiinflammatory, cytostatic, antipsoriatic, antidiabetic, and
CC   neuroprotective activity. The polynucleotides encoding the antibodies of
CC   the invention may have a use in gene therapy. The antibodies and
CC   polypeptides are useful for treating or preventing osteopathic diseases,
CC   such as rheumatoid arthritis, osteoporosis, metastatic and primary bone
CC   cancer, wear debris induced osteolysis or osteoarthritis, and immune
CC   diseases such as psoriasis, insulin-dependent diabetes, inflammatory
CC   bowel disease or multiple sclerosis. The present sequence represents the
CC   heavy chain variable region of the murine monoclonal antibody 14F3 of the
CC   invention. The sequence contains three complementary determining regions
CC   (CDR's)
XX
SQ   Sequence 134 AA;

  Query Match             78.0%;  Score 487;  DB 6;  Length 134;
  Best Local Similarity   79.3%;  Pred. No. 6e-38;
  Matches   96;  Conservative    6;  Mismatches   17;  Indels    2;  Gaps    1;

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Qy        119 S 119
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Db        121 S 121


RESULT 15
AAB20442
ID   AAB20442 standard; protein; 294 AA.
XX
AC   AAB20442;
XX
DT   21-JUN-2001  (first entry)
XX
DE   Anti-FIX/FIXa antibody 198/B1-myc-tag fusion.
XX
KW   Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant;
KW   Factor VIII cofactor; blood coagulation disorder; haemophilia A;
KW   haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse; myc-tag.
XX
OS   Mus musculus.
OS   Synthetic.
OS   Escherichia coli.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
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FT                   /label= Signal_peptide
FT   Protein         23. .294
FT                   /label= Mature_protein
FT   Protein         23. .271
FT                   /label= scFv
FT   Region          23. .144
FT                   /label= VH
FT   Misc-difference 76
FT                   /note= "encoded by GGN"
FT   Peptide         145. .159
FT                   /label= Linker
FT   Region          160. .271
FT                   /label= VL
FT   Peptide         272. .274
FT                   /label= Spacer
FT   Protein         275. .286
FT                   /label= Myc_tag
FT   Peptide         287. .288
FT                   /label= Spacer
FT   Peptide         289. .294
FT                   /label= His_tag
XX
PN   WO200119992-A2.
XX
PD   22-MAR-2001.
XX
PF   13-SEP-2000; 2000WO-EP008936.
XX
PR   14-SEP-1999;   99AT-00001576.
XX
PA   (BAXT ) BAXTER AG.
XX
PI   Scheiflinger F,  Kerschbaumer R,  Falkner F,  Dorner F;
XX
DR   WPI; 2001-290358/30.
DR   N-PSDB; AAF30732.
```

XX
PT New factor IX/factor IXa antibodies and their derivatives useful for
PT increasing amidolytic activity of factor IXa, and for treating blood
PT coagulation disorders such as hemophilia A and hemorrhagic diathesis.
XX
PS Example 18; Fig 34; 138pp; English.
XX
CC The present sequence is that of a fusion protein comprising: a PelB
CC leader; a single chain Fv (scFv) derivative of antibody 198/B1 comprising
CC the heavy (VH) and light (VL) chain variable regions of 198/B1 joined by
CC an artificial, flexible linker peptide; a spacer; a Myc-tag peptide; a
CC spacer; and a C-terminal 6His affinity tail. 198/B1 is an example of anti
CC -human Factor IX (FIX)/activated Factor IX (FIXa) antibodies of the
CC invention. Anti-FIX/FIXa antibodies and their derivatives, including scFv
CC fragments, have FVIIIa cofactor activity or FIXa activating activity.
CC Administration leads to an increase in the procoagulant activity of FIXa,
CC even in the presence of FVIIIa inhibitors. This allows for rapid blood
CC coagulation even in the absence of FVIII or FVIIIa, and in the case of
CC FVIII inhibitor patients. The antibodies and derivatives are used in a
CC claimed pharmaceutical composition for treating patients with blood
CC coagulation disorders, especially haemophilia A and haemorrhagic
CC diathesis. The scFv-myc-tag fusion was expressed in E. coli. It exhibited
CC FVIII-like activity
XX
SQ Sequence 294 AA;

Query Match 78.0%; Score 486.5; DB 4; Length 294;
Best Local Similarity 78.7%; Pred. No. 1.6e-37;
Matches 96; Conservative 6; Mismatches 17; Indels 3; Gaps 1;

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Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLG---TYYFDSWGQGTTLTV 117
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Qy        118 SS 119
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Db        143 SS 144
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Search completed: December 23, 2004, 18:57:39
Job time : 33.8339 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2004, 18:46:39 ; Search time 7.85924 Seconds
(without alignments)
1004.148 Million cell updates/sec

Title: US-10-089-500-55
Perfect score: 624
Sequence: 1 EVTLVESGGDFVKPGGSLKV.....KLGTYYFDSWGQGTTLTVSS 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	624	100.0	130	4	US-09-764-304-18	Sequence 18, Appl
3	614	98.4	130	4	US-09-225-322B-8	Sequence 8, Appli
4	614	98.4	130	4	US-09-764-304-8	Sequence 8, Appli
5	493	79.0	119	4	US-08-875-674A-1	Sequence 1, Appli
6	486	77.9	247	5	PCT-US94-07659-2	Sequence 2, Appli
7	480	76.9	119	4	US-08-875-674A-3	Sequence 3, Appli
8	472	75.6	239	2	US-08-553-497A-18	Sequence 18, Appl
9	469.5	75.2	135	3	US-08-579-378A-16	Sequence 16, Appl
10	466.5	74.8	118	1	US-08-326-362-2	Sequence 2, Appli
11	464	74.4	119	3	US-09-406-535-2	Sequence 2, Appli
12	460.5	73.8	124	4	US-09-518-737-2	Sequence 2, Appli
13	457.5	73.3	456	4	US-09-495-880A-11	Sequence 11, Appl
14	457	73.2	217	5	PCT-US94-14106-59	Sequence 59, Appl
15	453	72.6	119	4	US-09-648-067A-15	Sequence 15, Appl
16	452	72.4	119	1	US-08-497-312-20	Sequence 20, Appl
17	450.5	72.2	120	2	US-07-934-373C-4	Sequence 4, Appli
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29	447	71.6	119	1	US-08-331-398A-46	Sequence 46, Appl
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31	447	71.6	119	2	US-08-759-804A-46	Sequence 46, Appl
32	447	71.6	119	3	US-09-227-693-46	Sequence 46, Appl
33	447	71.6	123	3	US-09-344-587-13	Sequence 13, Appl
34	445.5	71.4	167	4	US-09-318-786-31	Sequence 31, Appl
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40	445	71.3	245	3	US-09-069-821-5	Sequence 5, Appli
41	445	71.3	245	4	US-09-956-086-5	Sequence 5, Appli
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44	444.5	71.2	247	6	5455030-9	Patent No. 5455030
45	444	71.2	125	2	US-08-428-197-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-225-322B-18
; Sequence 18, Application US/09225322B
; Patent No. 6437098
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/225,322B
; CURRENT FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:cDNA KM-641
US-09-225-322B-18

Query Match 100.0%; Score 624; DB 4; Length 130;
Best Local Similarity 100.0%; Pred. No. 8.8e-60;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-09-764-304-18
; Sequence 18, Application US/09764304

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; Patent No. 6495666
; GENERAL INFORMATION:
;  APPLICANT: SHITARA, KENYA
;  APPLICANT: HANAI, NOBUO
;  APPLICANT: HASEGAWA, MAMORU
;  APPLICANT: MIYAJI, HIROMASA
;  APPLICANT: KUWANA, YOSHIHISA
;  TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
;  FILE REFERENCE: 249-101
;  CURRENT APPLICATION NUMBER: US/09/764,304
;  CURRENT FILING DATE: 2001-01-19
;  EARLIER APPLICATION NUMBER: 09/225,322
;  EARLIER FILING DATE: 1999-01-05
;  EARLIER APPLICATION NUMBER: US 08/454,680
;  EARLIER FILING DATE: 1995-05-31
;  EARLIER APPLICATION NUMBER: US 08/408,133
;  EARLIER FILING DATE: 1995-03-21
;  EARLIER APPLICATION NUMBER: US 08/292,178
;  EARLIER FILING DATE: 1994-08-17
;  EARLIER APPLICATION NUMBER: US07/947,674
;  EARLIER FILING DATE: 1992-09-17
;  EARLIER APPLICATION NUMBER: JP 3-238375
;  EARLIER FILING DATE: 1991-09-18
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
;   LENGTH: 130
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: cDNA KM-641
US-09-764-304-18

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Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
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RESULT 3
US-09-225-322B-8
; Sequence 8, Application US/09225322B
; Patent No. 6437098
; GENERAL INFORMATION:
;  APPLICANT: SHITARA, KENYA
;  APPLICANT:  HANAI, NOBUO
;  APPLICANT:  HASEGAWA, MAMORU
;  APPLICANT:  MIYAJI, HIROMASA
;  APPLICANT:  KUWANA, YOSHIHISA
;  TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
;  FILE REFERENCE: 249-101
;  CURRENT APPLICATION NUMBER: US/09/225,322B
;  CURRENT FILING DATE:  1999-01-05
;  PRIOR APPLICATION NUMBER: US 08/454,680
;  PRIOR FILING DATE: 1995-05-31
;  PRIOR APPLICATION NUMBER: US 08/408,133
;  PRIOR FILING DATE: 1995-03-21
;  PRIOR APPLICATION NUMBER: US 08/292,178
;  PRIOR FILING DATE: 1994-08-17
;  PRIOR APPLICATION NUMBER: US07/947,674
;  PRIOR FILING DATE: 1992-09-17
;  PRIOR APPLICATION NUMBER: JP 3-238375
;  PRIOR FILING DATE: 1991-09-18
;  NUMBER OF SEQ ID NOS: 19
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; SEQ ID NO 8
;   LENGTH: 130
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;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-09-225-322B-8

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RESULT 4
US-09-764-304-8
; Sequence 8, Application US/09764304
; Patent No. 6495666
; GENERAL INFORMATION:
;  APPLICANT: SHITARA, KENYA
;  APPLICANT: HANAI, NOBUO
;  APPLICANT: HASEGAWA, MAMORU
;  APPLICANT: MIYAJI, HIROMASA
;  APPLICANT: KUWANA, YOSHIHISA
;  TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
;  FILE REFERENCE: 249-101
;  CURRENT APPLICATION NUMBER: US/09/764,304
;  CURRENT FILING DATE: 2001-01-19
;  EARLIER APPLICATION NUMBER: 09/225,322
;  EARLIER FILING DATE: 1999-01-05
;  EARLIER APPLICATION NUMBER: US 08/454,680
;  EARLIER FILING DATE: 1995-05-31
;  EARLIER APPLICATION NUMBER: US 08/408,133
;  EARLIER FILING DATE: 1995-03-21
;  EARLIER APPLICATION NUMBER: US 08/292,178
;  EARLIER FILING DATE: 1994-08-17
;  EARLIER APPLICATION NUMBER: US07/947,674
;  EARLIER FILING DATE: 1992-09-17
;  EARLIER APPLICATION NUMBER: JP 3-238375
;  EARLIER FILING DATE: 1991-09-18
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 130
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: cDNA KM-641
US-09-764-304-8

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  Matches  118;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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RESULT 5
US-08-875-674A-1
; Sequence 1, Application US/08875674A
; Patent No. 6572857
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;  GENERAL INFORMATION:
;    APPLICANT:  MONTERO  CASIMIRO, J. E.
;    APPLICANT:  LOMBARDERO  VALLADARES, J.
;    APPLICANT:  P REZ  RODR GUEZ, R.
;    APPLICANT:  SIERRA  BL ZQUEZ, P.
;    APPLICANT:  TORMO  BRAVO, B. R.
;    TITLE OF INVENTION:  Anti-CD6 monoclonal antibodies and their uses
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lackenbach Siegel Marzullo Aronson & Greenspan, P.C.
;      STREET:  One Chase Road
;      CITY:  Scarsdale
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10583
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk 3.5'' (1.4 MB).
;      COMPUTER:  Compatible PC IBM (80486, 8 M Ram).
;      OPERATING SYSTEM:  Windows 95.
;      SOFTWARE:  Word Perfect 5.0 for Windows 95.
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/875,674A
;      FILING DATE:  17-July-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/CU96/00004
;      FILING DATE:  18-NOV-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HENRY A. MARZULLO, JR.
;      REGISTRATION NUMBER:  20,910
;      REFERENCE/DOCKET NUMBER:  P-12
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (914) 723-4300
;      TELEFAX:  (914)-723-4301
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 Amino acid residues.
;      TYPE:  Amino acid.
;      STRANDEDNESS:  Unknown.
;      TOPOLOGY:  Unknown.
;    MOLECULE TYPE:  Protein
;    HYPOTHETICAL:  No
;    ANTI-SENSE:  No
;    FRAGMENT TYPE:  -N Terminal fragment.
;    ORIGINAL SOURCE:
;      ORGANISM:  Mice Balb/C
;      INDIVIDUAL ISOLATE:  ior t1A
;      TISSUE TYPE:  Murine hibridoma
;    IMMEDIATE SOURCE:
;      CLONE:  Sub-clone ior t1A
;    FEATURE:
;      IDENTIFICATION METHOD:  Experimental.
;      OTHER INFORMATION:  Sequence corresponding to the variable region
; Patent No. 6572857
;      OTHER INFORMATION:  of the heavy chain of the monoclonal antibody recognizing hum
;      OTHER INFORMATION:  designated as sub-clone ior t1A.
US-08-875-674A-1

  Query Match             79.0%;  Score 493;  DB 4;  Length 119;
  Best Local Similarity   81.5%;  Pred. No. 1e-45;
  Matches   97;  Conservative    3;  Mismatches   19;  Indels    0;  Gaps    0;

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Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
              |||||||||||| |||||||| ||||||:|||:|| |       ||||||||||||||
Db         61 PDSVKGRFTISRDNVKNTLYLQMSSLRSEDTAMYYCARRDYDLDYFDSWGQGTTLTVSS 119


RESULT 6
PCT-US94-07659-2
; Sequence 2, Application PC/TUS9407659
;  GENERAL INFORMATION:
;    APPLICANT:  Young, Peter
;    APPLICANT:  Gross, Mitchell
;    APPLICANT:  Jonak, Zdenka L.
;    APPLICANT:  Theisen, Timothy
;    APPLICANT:  Hurle, Mark
;    APPLICANT:  Jackson, Jeffrey R.
;    TITLE OF INVENTION:  Recombinant and Humanized Il-1 beta
;    TITLE OF INVENTION:  Antibodies for Treatment of Il-1 Mediated Inflammatory
;    TITLE OF INVENTION:  Disorders in Man
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SmithKline Beecham Corporation - Corp.
;      ADDRESSEE:  Intellectual Property
;      STREET:  709 Swedeland Road
;      CITY:  King of Prussia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19406-2799
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/07659
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/090,534
;      FILING DATE:  09-JUL-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sutton, Jeffrey A.
;      REGISTRATION NUMBER:  34,028
;      REFERENCE/DOCKET NUMBER:  P50171-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (610) 270-5024
;      TELEFAX:  (610) 270-5090
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  247 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US94-07659-2

  Query Match             77.9%;  Score 486;  DB 5;  Length 247;
  Best Local Similarity   79.0%;  Pred. No. 1.4e-44;
  Matches   94;  Conservative    7;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||  |||||||:|||||||||| | |||||||| |||:|||||||||| ||||
Db         20 EVHLVESGGGLVKPGGSLKLSCAASGFAFSSYDMSWVRQTPEKRLDWVAYISSGGGGTYY 79

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
              |:||||||||||||||||||| ||:|||:||| | |  :   ||| || |||:||||
Db         80 PDTVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYHCARGGVRRGYFDVWGAGTTVTVSS 138


RESULT 7
US-08-875-674A-3
; Sequence 3, Application US/08875674A
; Patent No. 6572857
;  GENERAL INFORMATION:
;    APPLICANT:  MONTERO  CASIMIRO, J. E.
;    APPLICANT:  LOMBARDERO  VALLADARES, J.
;    APPLICANT:  P REZ  RODR GUEZ, R.
;    APPLICANT:  SIERRA  BL ZQUEZ, P.
;    APPLICANT:  TORMO  BRAVO, B. R.
;    TITLE OF INVENTION:  Anti-CD6 monoclonal antibodies and their uses
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
```

```
;      ADDRESSEE:  Lackenbach Siegel Marzullo Aronson & Greenspan, P.C.
;      STREET:  One Chase Road
;      CITY:  Scarsdale
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10583
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk 3.5'' (1.4 MB).
;      COMPUTER:  Compatible PC IBM (80486, 8 M Ram).
;      OPERATING SYSTEM:  Windows 95.
;      SOFTWARE:  Word Perfect 5.0 for Windows 95.
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/875,674A
;      FILING DATE:  17-July-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/CU96/00004
;      FILING DATE:  18-NOV-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HENRY A. MARZULLO, JR.
;      REGISTRATION NUMBER:  20,910
;      REFERENCE/DOCKET NUMBER:  P-12
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (914) 723-4300
;      TELEFAX:  (914)-723-4301
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 Amino acid residues.
;      TYPE:  Amino acid.
;      STRANDEDNESS:  Unknown.
;      TOPOLOGY:  Unknown.
;    MOLECULE TYPE:  Protein
;    HYPOTHETICAL:  No
;    ANTI-SENSE:  No
;    FRAGMENT TYPE:  -N Terminal fragment.
;    ORIGINAL SOURCE:
;      TISSUE TYPE:  Animal cells.
;      CELL LINE:  NSO " SP 2/0 " CHO
;    IMMEDIATE SOURCE:
;      CLONE:  Sub-clone ior t1A
;    FEATURE:
;      IDENTIFICATION METHOD:  By similarity with known sequence.
;      OTHER INFORMATION:  Sequence corresponding to the humanized
; Patent No. 6572857
;      OTHER INFORMATION:  variant of sub-clone ior t1A recognizing human CD6, particula
;      OTHER INFORMATION:  to the variable region of its heavy chain.
US-08-875-674A-3

  Query Match             76.9%;  Score 480;  DB 4;  Length 119;
  Best Local Similarity   79.0%;  Pred. No. 2.6e-44;
  Matches   94;  Conservative    4;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||  |||||||:||||||| || |||||||| | ||||||| ||||||  ||
Db          1 EVQLVESGGGLVKPGGSLKLSCAASGFKFSRYAMSWVRQAPGKRLEWVATISSGGSYIYY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
               |||||||||||| |||||||| ||||||:|||:| |      ||||||||  :||||
Db         61 PDSVKGRFTISRDNVKNTLYLQMSSLRSEDTAMYYCARRDYDLDYFDSWGQGTLVTVSS 119


RESULT 8
US-08-553-497A-18
; Sequence 18, Application US/08553497A
; Patent No. 5844093
;  GENERAL INFORMATION:
;    APPLICANT:  KETTLEBOROUGH, C. A.
;    APPLICANT:  BENDIG, MARY M.
;    APPLICANT:  ANSELL, KEITH H.
;    APPLICANT:  GUSSOW, DETLEF
;    APPLICANT:  ADAN, JAUME
;    APPLICANT:  MITJANS, FRANSESC
;    APPLICANT:  ROSELL, ELISABET
;    APPLICANT:  BLASCO, FRANCESC
;    APPLICANT:  PIULATS, JAUME
;    TITLE OF INVENTION:  ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
;    TITLE OF INVENTION:  ANTIBODIES
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
;      STREET:  2200 CLARENDON BLVD. SUITE 1400
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  US
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/553,497A
;      FILING DATE:  17-NOV-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/EP95/00978
;      FILING DATE:  16-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 94104160.0
;      FILING DATE:  17-MAR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 94118970.6
;      FILING DATE:  02-DEC-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HAMLET-KING, DIANA
;      REGISTRATION NUMBER:  33,302
;      REFERENCE/DOCKET NUMBER:  MERCK 1726
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-243-6333
;      TELEFAX:  703-243-6410
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  239 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-553-497A-18

  Query Match             75.6%;  Score 472;  DB 2;  Length 239;
  Best Local Similarity   77.3%;  Pred. No. 4.4e-43;
  Matches   92;  Conservative    8;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || | ||||| ||||||||:||||||| || | |||||||| |||| || ||||||:  ||
Db          1 EVKLQESGGDLVKPGGSLKLSCAASGFTFSSYGMSWVRQTPDKRLESVATISSGGAYIYY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
               ||||||||||||||||||||| ||:|||:|||:| |:: | |  | ||||||:||||
Db         61 PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCARLETGDYALDYWGQGTTVTVSS 119


RESULT 9
US-08-579-378A-16
; Sequence 16, Application US/08579378A
; Patent No. 6210671
;  GENERAL INFORMATION:
;    APPLICANT:  Co, Man Sung
;    TITLE OF INVENTION:  Humanized Antibodies Reactive with
;    TITLE OF INVENTION:  L-Selectin
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew
;      STREET:  One MarketPlaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
```

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;       ZIP:  94105
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/579,378A
;       FILING DATE:  27-DEC-1995
;       CLASSIFICATION:  424
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/160,074
;       FILING DATE:  30-NOV-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/983,946
;       FILING DATE:  01-DEC-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  EP 95112895.8
;       FILING DATE:  17-AUG-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  EP 95114696.8
;       FILING DATE:  19-SEP-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Liebescheutz, Joe O.
;       REGISTRATION NUMBER:  37,505
;       REFERENCE/DOCKET NUMBER:  11823-002220
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-326-2400
;       TELEFAX:  415-326-2422
;   INFORMATION FOR SEQ ID NO:  16:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  135 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-579-378A-16

  Query Match             75.2%;  Score 469.5;  DB 3;  Length 135;
  Best Local Similarity   79.8%;  Pred. No. 4.1e-43;
  Matches   95;  Conservative    6;  Mismatches   15;  Indels    3;  Gaps    2;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || |||||| ||||||||::|||||| || |||||||||| ||||||| ||:||| |||
Db         20 EVKLVESGGGLVKPGGSLKLACAASGFTFSTYAMSWVRQTPEKRLEWVASISTGGS-TYY 78

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
              |||||||||||||:| ||||| ||||||:|||:| |    |  ||| ||||||||||
Db         79 PDSVKGRFTISRDNARNILYLQMSSLRSEDTAMYYCARDYDG--YFDYWGQGTTLTVSS 135


RESULT 10
US-08-326-362-2
; Sequence 2, Application US/08326362
; Patent No. 5730981
;  GENERAL INFORMATION:
;    APPLICANT:  Bosslet, Klaus
;    APPLICANT:  Seeman, Gerhard
;    APPLICANT:  Dippold, Wolfgang
;    TITLE OF INVENTION:  Monoclonal Anti-Ganglioside Antibody,
;    TITLE OF INVENTION:  Its Preparation and Use as a Tumortherapeutic Agent
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W., Suite 700
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/326,362
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/032,863
;      FILING DATE:  17-MAR-1993
;      APPLICATION NUMBER:  DE P 42 08 795.3
;      FILING DATE:  19-MAR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Einaudi, Carol P.
;      REGISTRATION NUMBER:  32,220
;      REFERENCE/DOCKET NUMBER:  02481-1276-00000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-408-4000
;      TELEFAX:  202-408-4400
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  118 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-326-362-2

  Query Match             74.8%;  Score 466.5;  DB 1;  Length 118;
  Best Local Similarity   77.3%;  Pred. No. 7.3e-43;
  Matches   92;  Conservative    7;  Mismatches   19;  Indels    1;  Gaps    1;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              :| | :|||  ||||||| :||||| | || ||||||||||||||||||||||||: |||
Db          1 QVQLQQSGGGLVKPGGSLTLSCAASRFTFSTYAMSWVRQTPAKRLEWVAYISSGGASTYY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
              ||||||||||||||||||||| ||||||:|||:| |      |  | ||||||:||||
Db         61 RDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCARGG-SRYAMDYWGQGTTVTVSS 118


RESULT 11
US-09-406-535-2
; Sequence 2, Application US/09406535
; Patent No. 6376653
; GENERAL INFORMATION:
;  APPLICANT: Connie L. Erickson-Miller
;  APPLICANT: Stephen D. Holmes
;  APPLICANT: James D. Winkler
;  TITLE OF INVENTION: Tie2 Antagonist Antibodies
;  FILE REFERENCE: P50844
;  CURRENT APPLICATION NUMBER: US/09/406,535
;  CURRENT FILING DATE: 1999-09-27
;  EARLIER APPLICATION NUMBER: 60/102,100
;  EARLIER FILING DATE: 1998-09-28
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-406-535-2

  Query Match             74.4%;  Score 464;  DB 3;  Length 119;
  Best Local Similarity   74.8%;  Pred. No. 1.4e-42;
  Matches   89;  Conservative    8;  Mismatches   22;  Indels    0;  Gaps    0;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || |||||| ||||||||:||||||| || | | |||| | | |||||||:|| |   |
Db          1 EVQLVESGGGLVKPGGSLKLSCAASGFTFSDYGMHWVRQAPEKGLEWVAYINSGSSTITY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
              :|:|||||||||||||||:||| ||||||:|:|:| |    | |||| ||||| |||||
Db         61 ADTVKGRFTISRDNAKNTLFLQMTSLRSEDTAIYYCARGYYGPYYFDYWGQGTALTVSS 119
```

```
RESULT 12
US-09-518-737-2
; Sequence 2, Application US/09518737
; Patent No. 6709833
; GENERAL INFORMATION:
;  APPLICANT: FUKUI, YASUHISA
;  APPLICANT:  NAGATA, SATOSHI
;  APPLICANT:  SHIRAI, RYUICHI
;  APPLICANT:  SAITO, NAOAKI
;  TITLE OF INVENTION: MONOCLONAL ANTIBODY RECOGNIZING
;  TITLE OF INVENTION:  PHOSPHATIDYLINOSITOL-3,4-DIPHOSPHATE
;  FILE REFERENCE: 1965/49618
;  CURRENT APPLICATION NUMBER: US/09/518,737
;  CURRENT FILING DATE:  2000-03-03
;  PRIOR APPLICATION NUMBER: JP 1999-250209
;  PRIOR FILING DATE: 1999-09-03
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 124
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-518-737-2

  Query Match             73.8%;  Score 460.5;  DB 4;  Length 124;
  Best Local Similarity   74.8%;  Pred. No. 3.4e-42;
  Matches   92;  Conservative    7;  Mismatches   17;  Indels    7;  Gaps    2;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||| ||||||:|:||||||| || | ||| |||| ||||||| |||||| |||
Db          1 EVQLVESGGDLVKPGGSVKLSCAASGFTFSSYGMSWARQTPDKRLEWVASISSGGSYTYY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTR----VKLGTYYFDSWGQGTTLT 116
              |||||||||||||||||||| ||:|||:|||:| |    |  |   |    ||||| :|
Db         61 PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCARQRGYVNFGIAY---WGQGTLVT 117

Qy        117 VSS 119
              |||
Db        118 VSA 120


RESULT 13
US-09-495-880A-11
; Sequence 11, Application US/09495880A
; Patent No. 6667150
; GENERAL INFORMATION:
;  APPLICANT: RUDERT, FRITZ
;  APPLICANT:  GE, LIMING
;  APPLICANT:  ILAG, VIC
;  TITLE OF INVENTION: NOVEL METHOD AND PHAGE FOR THE IDENTIFICATION OF
;  TITLE OF INVENTION:  NUCLEIC ACID SEQUENCES ENCODING MEMBERS OF A MULTIMERIC
;  TITLE OF INVENTION:  (POLY)PEPTIDE COMPLEX
;  FILE REFERENCE: MORPHO/9
;  CURRENT APPLICATION NUMBER: US/09/495,880A
;  CURRENT FILING DATE:  2000-02-01
;  PRIOR APPLICATION NUMBER: PCT/EP98/04836
;  PRIOR FILING DATE: 1998-08-03
;  PRIOR APPLICATION NUMBER: EP 97 11 3319.4
;  PRIOR FILING DATE: 1997-08-01
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
;   LENGTH: 456
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: ompA-FLAG-scFv (anti-
;   OTHER INFORMATION: HAG)-gene IIIss encoded by phage vector fhag1A (circular)
US-09-495-880A-11

  Query Match             73.3%;  Score 457.5;  DB 4;  Length 456;
  Best Local Similarity   75.8%;  Pred. No. 3.6e-41;
  Matches   91;  Conservative    8;  Mismatches   20;  Indels    1;  Gaps    1;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||| |||||||:|||||||:|| | |||||||| ||||||| ||:||  |||
Db        170 EVQLVESGGDLVKPGGSLKLSCAASGFSFSSYGMSWVRQTPDKRLEWVATISNGGGYTYY 229

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCT-RVKLGTYYFDSWGQGTTLTVSS 119
              |||||||||||||||||||| ||:|||||||:|  | :     |  ||||| :|||:
Db        230 PDSVKGRFTISRDNAKNTLYLQMSSLKSEDSAMYYCARRERYDENGFAYWGQGTLVTVSA 289


RESULT 14
PCT-US94-14106-59
; Sequence 59, Application PC/TUS9414106
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Process for Generating Specific Antibodies
;    NUMBER OF SEQUENCES:  61
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII (text)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/14106
;      FILING DATE:
;      CLASSIFICATION:
;  INFORMATION FOR SEQ ID NO:  59:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  217 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US94-14106-59

  Query Match             73.2%;  Score 457;  DB 5;  Length 217;
  Best Local Similarity   75.6%;  Pred. No. 1.6e-41;
  Matches   90;  Conservative    8;  Mismatches   17;  Indels    4;  Gaps    1;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || |:||||| |||||||:||||||| || | | |||||| ||||||| ||  |: |||
Db          1 EVKLMESGGDLVKPGGSLKLSCAASGFTFSDYYMYWVRQTPEKRLEWVATISDDGTYTYY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
              :|||||||||||||| ||||| ||:|||:|||:| |  |    : ||||||||||||
Db         61 ADSVKGRFTISRDNAKNNLYLQMNSLKSEDTAMYYCARDPL----YGSWGQGTTLTVSS 115


RESULT 15
US-09-648-067A-15
; Sequence 15, Application US/09648067A
; Patent No. 6627196
; GENERAL INFORMATION:
;  APPLICANT:  Baughman, Sharon A.
;  APPLICANT:  Shak Steven
;  TITLE OF INVENTION:  Dosages for Treatment with Anti-ErbB2 Antibodies
;  FILE REFERENCE:  P1775R1
;  CURRENT APPLICATION NUMBER: US/09/648,067A
;  CURRENT FILING DATE:  2000-08-25
;  PRIOR APPLICATION NUMBER:  US 60/151,018
;  PRIOR FILING DATE:  1999-08-27
;  PRIOR APPLICATION NUMBER:  US 60/213,822
;  PRIOR FILING DATE:  2000-06-23
;  NUMBER OF SEQ ID NOS:  15
; SEQ ID NO 15
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: VH consensus sequence
US-09-648-067A-15

  Query Match             72.6%;  Score 453;  DB 4;  Length 119;
  Best Local Similarity   71.4%;  Pred. No. 2.1e-41;
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Matches 85; Conservative 13; Mismatches 21; Indels 0; Gaps 0;

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Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||  |:|||||::|||||||  || ||||||||  |  |  |||||  ||   |  |||
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Search completed: December 23, 2004, 19:08:01
Job time : 8.85924 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2004, 19:04:51 ; Search time 27.0707 Seconds
(without alignments)
1578.640 Million cell updates/sec

Title: US-10-089-500-55
Perfect score: 624
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1595201 seqs, 359116952 residues

Total number of hits satisfying chosen parameters: 1595201

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	624	100.0	130	14	US-10-265-713-18	Sequence 18, Appl
3	624	100.0	130	14	US-10-166-626-18	Sequence 18, Appl
4	614	98.4	130	9	US-09-764-304-8	Sequence 8, Appli
5	614	98.4	130	14	US-10-265-713-8	Sequence 8, Appli
6	614	98.4	130	14	US-10-166-626-8	Sequence 8, Appli
7	487	78.0	134	17	US-10-477-377-3	Sequence 3, Appli
8	486	77.9	140	13	US-10-006-773-4	Sequence 4, Appli
9	481	77.1	121	14	US-10-276-939-3	Sequence 3, Appli
10	475	76.1	119	14	US-10-281-479A-61	Sequence 61, Appl
11	475	76.1	119	14	US-10-275-180A-61	Sequence 61, Appl
12	475	76.1	119	14	US-10-286-132A-61	Sequence 61, Appl
13	475	76.1	462	14	US-10-281-479A-23	Sequence 23, Appl
14	475	76.1	462	14	US-10-286-132A-23	Sequence 23, Appl
15	475	76.1	464	14	US-10-275-180A-23	Sequence 23, Appl
16	473.5	75.9	120	15	US-10-412-406-2	Sequence 2, Appli
17	473.5	75.9	4852	15	US-10-412-406-33	Sequence 33, Appl
18	473	75.8	123	9	US-09-144-886-61	Sequence 61, Appl
19	473	75.8	123	16	US-10-632-706-58	Sequence 58, Appl
20	471	75.5	119	14	US-10-270-071-5	Sequence 5, Appli
21	471	75.5	119	14	US-10-270-071-6	Sequence 6, Appli
22	471	75.5	262	14	US-10-270-071-20	Sequence 20, Appl
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25	471	75.5	268	14	US-10-270-071-10	Sequence 10, Appl
26	471	75.5	268	14	US-10-270-071-12	Sequence 12, Appl
27	471	75.5	268	14	US-10-270-071-14	Sequence 14, Appl
28	471	75.5	268	14	US-10-270-071-16	Sequence 16, Appl
29	471	75.5	415	14	US-10-328-190-12	Sequence 12, Appl
30	469	75.2	262	14	US-10-270-071-34	Sequence 34, Appl
31	469	75.2	268	14	US-10-270-071-32	Sequence 32, Appl
32	469	75.2	268	14	US-10-328-190-2	Sequence 2, Appli
33	469	75.2	268	14	US-10-328-190-4	Sequence 4, Appli
34	468.5	75.1	118	9	US-09-423-800-46	Sequence 46, Appl
35	468.5	75.1	118	14	US-10-182-018-46	Sequence 46, Appl
36	468.5	75.1	118	14	US-10-169-003-46	Sequence 46, Appl
37	468.5	75.1	118	14	US-10-337-981-46	Sequence 46, Appl
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40	468.5	75.1	137	14	US-10-337-981-76	Sequence 76, Appl
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42	468	75.0	125	11	US-09-910-358D-8	Sequence 8, Appli
43	468	75.0	140	9	US-09-286-240-4	Sequence 4, Appli
44	468	75.0	144	9	US-09-881-823-12	Sequence 12, Appl
45	468	75.0	155	14	US-10-077-624-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-764-304-18
; Sequence 18, Application US/09764304
; Patent No. US20020026036A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; CURRENT FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cDNA KM-641
US-09-764-304-18

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  Matches  119;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
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RESULT 2
US-10-265-713-18
; Sequence 18, Application US/10265713
; Publication No. US20030095964A1
; GENERAL INFORMATION:
;  APPLICANT: SHITARA, KENYA
;  APPLICANT:  HANAI, NOBUO
;  APPLICANT:  HASEGAWA, MAMORU
;  APPLICANT:  MIYAJI, HIROMASA
;  APPLICANT:  KUWANA, YOSHIHISA
;  TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
;  FILE REFERENCE: 249-101
;  CURRENT APPLICATION NUMBER: US/10/265,713
;  CURRENT FILING DATE:  2002-10-08
;  PRIOR APPLICATION NUMBER: US/09/225,322
;  PRIOR FILING DATE: 1999-01-05
;  PRIOR APPLICATION NUMBER: US 08/454,680
;  PRIOR FILING DATE: 1995-05-31
;  PRIOR APPLICATION NUMBER: US 08/408,133
;  PRIOR FILING DATE: 1995-03-21
;  PRIOR APPLICATION NUMBER: US 08/292,178
;  PRIOR FILING DATE: 1994-08-17
;  PRIOR APPLICATION NUMBER: US07/947,674
;  PRIOR FILING DATE: 1992-09-17
;  PRIOR APPLICATION NUMBER: JP 3-238375
;  PRIOR FILING DATE: 1991-09-18
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
;   LENGTH: 130
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:cDNA KM-641
US-10-265-713-18

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RESULT 3
US-10-166-626-18
; Sequence 18, Application US/10166626
; Publication No. US20030166876A1
; GENERAL INFORMATION:
;  APPLICANT: SHITARA, KENYA
;  APPLICANT:  HANAI, NOBUO
;  APPLICANT:  HASEGAWA, MAMORU
;  APPLICANT:  MIYAJI, HIROMASA
;  APPLICANT:  KUWANA, YOSHIHISA
;  TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
;  FILE REFERENCE: 249-101
;  CURRENT APPLICATION NUMBER: US/10/166,626
;  CURRENT FILING DATE:  2002-06-12
;  PRIOR APPLICATION NUMBER: US/09/225,322B
;  PRIOR FILING DATE: 1999-01-05
;  PRIOR APPLICATION NUMBER: US 08/454,680
;  PRIOR FILING DATE: 1995-05-31
;  PRIOR APPLICATION NUMBER: US 08/408,133
;  PRIOR FILING DATE: 1995-03-21
;  PRIOR APPLICATION NUMBER: US 08/292,178
;  PRIOR FILING DATE: 1994-08-17
;  PRIOR APPLICATION NUMBER: US07/947,674
;  PRIOR FILING DATE: 1992-09-17
;  PRIOR APPLICATION NUMBER: JP 3-238375
;  PRIOR FILING DATE: 1991-09-18
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
;   LENGTH: 130
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:cDNA KM-641
US-10-166-626-18

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RESULT 4
US-09-764-304-8
; Sequence 8, Application US/09764304
; Patent No. US20020026036A1
; GENERAL INFORMATION:
;  APPLICANT: SHITARA, KENYA
;  APPLICANT: HANAI, NOBUO
;  APPLICANT: HASEGAWA, MAMORU
;  APPLICANT: MIYAJI, HIROMASA
;  APPLICANT: KUWANA, YOSHIHISA
;  TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
;  FILE REFERENCE: 249-101
;  CURRENT APPLICATION NUMBER: US/09/764,304
;  CURRENT FILING DATE: 2001-01-19
;  EARLIER APPLICATION NUMBER: 09/225,322
;  EARLIER FILING DATE: 1999-01-05
;  EARLIER APPLICATION NUMBER: US 08/454,680
;  EARLIER FILING DATE: 1995-05-31
;  EARLIER APPLICATION NUMBER: US 08/408,133
;  EARLIER FILING DATE: 1995-03-21
;  EARLIER APPLICATION NUMBER: US 08/292,178
;  EARLIER FILING DATE: 1994-08-17
;  EARLIER APPLICATION NUMBER: US07/947,674
;  EARLIER FILING DATE: 1992-09-17
;  EARLIER APPLICATION NUMBER: JP 3-238375
;  EARLIER FILING DATE: 1991-09-18
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;  SOFTWARE: PatentIn Ver. 2.0
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US-09-764-304-8
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US-10-265-713-8
; Sequence 8, Application US/10265713
; Publication No. US20030095964A1
; GENERAL INFORMATION:
;  APPLICANT: SHITARA, KENYA
;  APPLICANT:  HANAI, NOBUO
;  APPLICANT:  HASEGAWA, MAMORU
;  APPLICANT:  MIYAJI, HIROMASA
;  APPLICANT:  KUWANA, YOSHIHISA
;  TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
;  FILE REFERENCE: 249-101
;  CURRENT APPLICATION NUMBER: US/10/265,713
;  CURRENT FILING DATE:  2002-10-08
;  PRIOR APPLICATION NUMBER: US/09/225,322
;  PRIOR FILING DATE: 1999-01-05
;  PRIOR APPLICATION NUMBER: US 08/454,680
;  PRIOR FILING DATE: 1995-05-31
;  PRIOR APPLICATION NUMBER: US 08/408,133
;  PRIOR FILING DATE: 1995-03-21
;  PRIOR APPLICATION NUMBER: US 08/292,178
;  PRIOR FILING DATE: 1994-08-17
;  PRIOR APPLICATION NUMBER: US07/947,674
;  PRIOR FILING DATE: 1992-09-17
;  PRIOR APPLICATION NUMBER: JP 3-238375
;  PRIOR FILING DATE: 1991-09-18
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 130
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-10-265-713-8

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RESULT 6
US-10-166-626-8
; Sequence 8, Application US/10166626
; Publication No. US20030166876A1
; GENERAL INFORMATION:
;  APPLICANT: SHITARA, KENYA
;  APPLICANT:  HANAI, NOBUO
;  APPLICANT:  HASEGAWA, MAMORU
;  APPLICANT:  MIYAJI, HIROMASA
;  APPLICANT:  KUWANA, YOSHIHISA
;  TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
;  FILE REFERENCE: 249-101
;  CURRENT APPLICATION NUMBER: US/10/166,626
;  CURRENT FILING DATE:  2002-06-12
;  PRIOR APPLICATION NUMBER: US/09/225,322B
;  PRIOR FILING DATE: 1999-01-05
;  PRIOR APPLICATION NUMBER: US 08/454,680
;  PRIOR FILING DATE: 1995-05-31
;  PRIOR APPLICATION NUMBER: US 08/408,133
;  PRIOR FILING DATE: 1995-03-21
;  PRIOR APPLICATION NUMBER: US 08/292,178
;  PRIOR FILING DATE: 1994-08-17
;  PRIOR APPLICATION NUMBER: US07/947,674
;  PRIOR FILING DATE: 1992-09-17
;  PRIOR APPLICATION NUMBER: JP 3-238375
;  PRIOR FILING DATE: 1991-09-18
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 130
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-10-166-626-8

  Query Match             98.4%;  Score 614;  DB 14;  Length 130;
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  Matches  118;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
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RESULT 7
US-10-477-377-3
; Sequence 3, Application US/10477377
; Publication No. US20040213788A1
; GENERAL INFORMATION:
;  APPLICANT: Sweet, Raymond
;  APPLICANT:  Tornetta, Mark
;  APPLICANT:  Wattam, Trevor
;  TITLE OF INVENTION: Anti-RANK Ligand Monoclonal Antibodies
;  TITLE OF INVENTION:  Useful in Treatment of RANK Ligand Mediated Disorders
;  FILE REFERENCE: GP50050
;  CURRENT APPLICATION NUMBER: US/10/477,377
;  CURRENT FILING DATE:  2003-11-12
;  PRIOR APPLICATION NUMBER: PCT/US02/14246
;  PRIOR FILING DATE: 2002-05-03
;  PRIOR APPLICATION NUMBER: 60/292,031
;  PRIOR FILING DATE: 2001-05-18
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
;   LENGTH: 134
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-477-377-3

  Query Match             78.0%;  Score 487;  DB 17;  Length 134;
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Qy        119 S 119
              |
Db        121 S 121


RESULT 8
US-10-006-773-4
; Sequence 4, Application US/10006773
; Publication No. US20020132983A1
; GENERAL INFORMATION:
;  APPLICANT: Junghans, Richard P.
;  TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Anti
;  FILE REFERENCE: 003
;  CURRENT APPLICATION NUMBER: US/10/006,773
;  CURRENT FILING DATE:  2001-12-10
;  PRIOR APPLICATION NUMBER: 60/250,089
;  PRIOR FILING DATE: 2000-11-30
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 140
;   TYPE: PRT
;   ORGANISM: Mus sp.
US-10-006-773-4

  Query Match             77.9%;  Score 486;  DB 13;  Length 140;
  Best Local Similarity   77.7%;  Pred. No. 1.9e-37;
  Matches   94;  Conservative    9;  Mismatches   16;  Indels    2;  Gaps    1;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || :||||| |||||||||:||||:|| || |||||||||| ||||||| |||||| |||
Db         20 EVVVVESGGGFVKPGGSLKLSCAAAGFTFSRYAMSWVRQTPEKRLEWVATISSGGSHTYY 79

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTR--VKLGTYYFDSWGQGTTLTVS 118
              |||||||||||||||||||| |||||||:|:|:| |     | ::||| || |||:|||
Db         80 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAIYYCARPGYDRGAWFFDVWGAGTTVTVS 139

Qy        119 S 119
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Db        140 S 140


RESULT 9
US-10-276-939-3
; Sequence 3, Application US/10276939
; Publication No. US20030215450A1
; GENERAL INFORMATION:
;  APPLICANT: BLAKE, SIMON M.
;  APPLICANT:  SWEET, RAYMOND W.
;  APPLICANT:  TAYLOR, ALEXANDER H.
;  APPLICANT:  WATTAM, TREVOR A.
;  TITLE OF INVENTION: Anti-RANK Ligand Monoclonal Antibodies
;  TITLE OF INVENTION:  Useful in Treatment of RANK Ligand Mediated Disorders
;  FILE REFERENCE: GP50024
;  CURRENT APPLICATION NUMBER: US/10/276,939
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: PCT/US01/16865
;  PRIOR FILING DATE: 2001-05-24
;  PRIOR APPLICATION NUMBER: 60/207,628
;  PRIOR FILING DATE: 2000-05-26
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
;   LENGTH: 121
;   TYPE: PRT
;   ORGANISM: Murine
US-10-276-939-3

  Query Match             77.1%;  Score 481;  DB 14;  Length 121;
  Best Local Similarity   78.5%;  Pred. No. 4.7e-37;
  Matches   95;  Conservative    6;  Mismatches   18;  Indels    2;  Gaps    1;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||| ||||||||:||||||| || | |||||||| ||||||| ||||||  ||
Db          1 EVQLVESGGDLVKPGGSLKLSCAASGFTFSRYGMSWVRQTPDKRLEWVATISSGGSYIYY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTY--YFDSWGQGTTLTVS 118
              |||||||||||||||||||| ||:|||:|||:| |:    |  ||| || |||:|||
Db         61 PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCARLDGYNYRWYFDVWGTGTTVTVS 120

Qy        119 S 119
              |
Db        121 S 121


RESULT 10
US-10-281-479A-61
; Sequence 61, Application US/10281479A
; Publication No. US20030133932A1
; GENERAL INFORMATION:
;  APPLICANT: The UAB Research Foundation
;  APPLICANT:  Zhou, Tong
;  APPLICANT:  Ichikawa, Kimihisa
;  APPLICANT:  Kimberly, Robert P.
;  APPLICANT:  Koopman, William J.
;  APPLICANT:  Oshumi, Jun
;  APPLICANT:  LoBuglio, Albert S.
;  APPLICANT:  Buchsbaum, Donald J.
;  TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
;  TITLE OF INVENTION:  FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THER
;  TITLE OF INVENTION:  AGENTS
;  FILE REFERENCE: 21085.0029U6
;  CURRENT APPLICATION NUMBER: US/10/281,479A
;  CURRENT FILING DATE:  2003-01-28
;  PRIOR APPLICATION NUMBER: 60/391,478
;  PRIOR FILING DATE: 2002-06-24
;  PRIOR APPLICATION NUMBER: 60/346,402
;  PRIOR FILING DATE: 2001-11-01
;  PRIOR APPLICATION NUMBER: PCT/US01/14151
;  PRIOR FILING DATE: 2001-05-02
;  PRIOR APPLICATION NUMBER: 60/201,344
;  PRIOR FILING DATE: 2000-05-02
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 61
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/No. US20030133932A1e = Synthe
US-10-281-479A-61

  Query Match             76.1%;  Score 475;  DB 14;  Length 119;
  Best Local Similarity   79.8%;  Pred. No. 1.7e-36;
  Matches   95;  Conservative    3;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||  |||||||:||||||| || | |||||||| ||||||| |||||| |||
Db          1 EVMLVESGGGLVKPGGSLKLSCAASGFTFSSYVMSWVRQTPEKRLEWVATISSGGSYTYY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
              ||||||||||||||||||||| ||||||:|||:| |         | ||||||||||
Db         61 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCARRGDSMITTDYWGQGTTLTVSS 119


RESULT 11
US-10-275-180A-61
; Sequence 61, Application US/10275180A
; Publication No. US20030190687A1
; GENERAL INFORMATION:
;  APPLICANT: The UAB Research Foundation
;  APPLICANT:  Zhou, Tong
;  APPLICANT:  Ichikawa, Kimihisa
```

```
;  APPLICANT:  Kimberly, Robert P.
;  APPLICANT:  Koopman, William J.
;  TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPTOS
;  TITLE OF INVENTION:  INDUCING LIGAND RECEPTOR AND USES THEREOF
;  FILE REFERENCE: 21085.0029U5
;  CURRENT APPLICATION NUMBER: US/10/275,180A
;  CURRENT FILING DATE:  2002-10-31
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 61
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/No. US20030190687A1e =
;   OTHER INFORMATION: Synthetic Construct
US-10-275-180A-61

  Query Match             76.1%;  Score 475;  DB 14;  Length 119;
  Best Local Similarity   79.8%;  Pred. No. 1.7e-36;
  Matches   95;  Conservative    3;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||  ||||||||:||||||| || | |||||||| ||||||| |||||| |||
Db          1 EVMLVESGGGLVKPGGSLKLSCAASGFTFSSYVMSWVRQTPEKRLEWVATISSGGSYTYY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
              ||||||||||||||||||||||| ||||||:|||:| |         | ||||||||||
Db         61 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCARRGDSMITTDYWGQGTTLTVSS 119


RESULT 12
US-10-286-132A-61
; Sequence 61, Application US/10286132A
; Publication No. US20030198637A1
; GENERAL INFORMATION:
;  APPLICANT: Zhou, Tong
;  APPLICANT:  Kimberly, Robert P.
;  APPLICANT:  Koopman, William J.
;  APPLICANT:  LoBuglio, Albert S.
;  APPLICANT:  Buchsbaum, Donald J.
;  TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED
;  TITLE OF INVENTION:  APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF
;  FILE REFERENCE: 21085.0029U7
;  CURRENT APPLICATION NUMBER: US/10/286,132A
;  CURRENT FILING DATE:  2003-01-22
;  PRIOR APPLICATION NUMBER: US 60/346,402
;  PRIOR FILING DATE: 2001-11-01
;  PRIOR APPLICATION NUMBER: PCT/US01/14151
;  PRIOR FILING DATE: 2001-05-02
;  PRIOR APPLICATION NUMBER: US 60/201,344
;  PRIOR FILING DATE: 2000-05-02
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 61
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/No. US20030198637A1e = Synthe
US-10-286-132A-61

  Query Match             76.1%;  Score 475;  DB 14;  Length 119;
  Best Local Similarity   79.8%;  Pred. No. 1.7e-36;
  Matches   95;  Conservative    3;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||  ||||||||:||||||| || | |||||||| ||||||| |||||| |||
Db          1 EVMLVESGGGLVKPGGSLKLSCAASGFTFSSYVMSWVRQTPEKRLEWVATISSGGSYTYY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
              ||||||||||||||||||||||| ||||||:|||:| |         | ||||||||||
Db         61 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCARRGDSMITTDYWGQGTTLTVSS 119


RESULT 13
US-10-281-479A-23
; Sequence 23, Application US/10281479A
; Publication No. US20030133932A1
; GENERAL INFORMATION:
;  APPLICANT: The UAB Research Foundation
;  APPLICANT:  Zhou, Tong
;  APPLICANT:  Ichikawa, Kimihisa
;  APPLICANT:  Kimberly, Robert P.
;  APPLICANT:  Koopman, William J.
;  APPLICANT:  Oshumi, Jun
;  APPLICANT:  LoBuglio, Albert S.
;  APPLICANT:  Buchsbaum, Donald J.
;  TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
;  TITLE OF INVENTION:  FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THE
;  TITLE OF INVENTION:  AGENTS
;  FILE REFERENCE: 21085.0029U6
;  CURRENT APPLICATION NUMBER: US/10/281,479A
;  CURRENT FILING DATE:  2003-01-28
;  PRIOR APPLICATION NUMBER: 60/391,478
;  PRIOR FILING DATE: 2002-06-24
;  PRIOR APPLICATION NUMBER: 60/346,402
;  PRIOR FILING DATE: 2001-11-01
;  PRIOR APPLICATION NUMBER: PCT/US01/14151
;  PRIOR FILING DATE: 2001-05-02
;  PRIOR APPLICATION NUMBER: 60/201,344
;  PRIOR FILING DATE: 2000-05-02
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
;   LENGTH: 462
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/No. US20030133932A1e = Synth
US-10-281-479A-23

  Query Match             76.1%;  Score 475;  DB 14;  Length 462;
  Best Local Similarity   79.8%;  Pred. No. 6.8e-36;
  Matches   95;  Conservative    3;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||  ||||||||:||||||| || | |||||||| ||||||| |||||| |||
Db         20 EVMLVESGGGLVKPGGSLKLSCAASGFTFSSYVMSWVRQTPEKRLEWVATISSGGSYTYY 79

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
              ||||||||||||||||||||||| ||||||:|||:| |         | ||||||||||
Db         80 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCARRGDSMITTDYWGQGTTLTVSS 138


RESULT 14
US-10-286-132A-23
; Sequence 23, Application US/10286132A
; Publication No. US20030198637A1
; GENERAL INFORMATION:
;  APPLICANT: Zhou, Tong
;  APPLICANT:  Kimberly, Robert P.
;  APPLICANT:  Koopman, William J.
;  APPLICANT:  LoBuglio, Albert S.
;  APPLICANT:  Buchsbaum, Donald J.
;  TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED
;  TITLE OF INVENTION:  APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF
;  FILE REFERENCE: 21085.0029U7
;  CURRENT APPLICATION NUMBER: US/10/286,132A
;  CURRENT FILING DATE:  2003-01-22
;  PRIOR APPLICATION NUMBER: US 60/346,402
;  PRIOR FILING DATE: 2001-11-01
;  PRIOR APPLICATION NUMBER: PCT/US01/14151
;  PRIOR FILING DATE: 2001-05-02
;  PRIOR APPLICATION NUMBER: US 60/201,344
;  PRIOR FILING DATE: 2000-05-02
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;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
;   LENGTH: 462
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/No. US20030198637A1e = Synthe
US-10-286-132A-23

  Query Match             76.1%;  Score 475;  DB 14;  Length 462;
  Best Local Similarity   79.8%;  Pred. No. 6.8e-36;
  Matches   95;  Conservative    3;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||  ||||||||:||||||| || | |||||||| ||||||| |||||| |||
Db         20 EVMLVESGGGLVKPGGSLKLSCAASGFTFSSYVMSWVRQTPEKRLEWVATISSGGSYTYY 79

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
              |||||||||||||||||||| ||||||:|||:| |         | ||||||||||
Db         80 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCARRGDSMITTDYWGQGTTLTVSS 138


RESULT 15
US-10-275-180A-23
; Sequence 23, Application US/10275180A
; Publication No. US20030190687A1
; GENERAL INFORMATION:
;  APPLICANT: The UAB Research Foundation
;  APPLICANT:  Zhou, Tong
;  APPLICANT:  Ichikawa, Kimihisa
;  APPLICANT:  Kimberly, Robert P.
;  APPLICANT:  Koopman, William J.
;  TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPTOS
;  TITLE OF INVENTION:  INDUCING LIGAND RECEPTOR AND USES THEREOF
;  FILE REFERENCE: 21085.0029U5
;  CURRENT APPLICATION NUMBER: US/10/275,180A
;  CURRENT FILING DATE:  2002-10-31
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
;   LENGTH: 464
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/No. US20030190687A1e =
;   OTHER INFORMATION: Synthetic Construct
US-10-275-180A-23

  Query Match             76.1%;  Score 475;  DB 14;  Length 464;
  Best Local Similarity   79.8%;  Pred. No. 6.8e-36;
  Matches   95;  Conservative    3;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||  ||||||||:||||||| || | |||||||| ||||||| |||||| |||
Db         20 EVMLVESGGGLVKPGGSLKLSCAASGFTFSSYVMSWVRQTPEKRLEWVATISSGGSYTYY 79

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
              |||||||||||||||||||| ||||||:|||:| |         | ||||||||||
Db         80 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCARRGDSMITTDYWGQGTTLTVSS 138


Search completed: December 23, 2004, 19:35:48
Job time : 28.0707 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2004, 18:46:03 ; Search time 6.43029 Seconds
(without alignments)
1780.604 Million cell updates/sec

Title: US-10-089-500-55
Perfect score: 624
Sequence: 1 EVTLVESGGDFVKPGGSLKV.....KLGTYYFDSWGQGTTLTVSS 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	479	76.8	119	2	B34353	anti-peptide Fab'
2	471	75.5	120	2	S55536	Ig heavy chain V r
3	470.5	75.4	121	2	I27887	Ig heavy chain V r
4	469	75.2	120	2	S55537	Ig heavy chain V r
5	469	75.2	122	2	E27888	Ig heavy chain V r
6	467	74.8	111	2	PH1007	Ig heavy chain V r
7	466.5	74.8	119	2	F27888	Ig heavy chain V r
8	464	74.4	138	2	S09258	Ig heavy chain V r
9	463	74.2	120	2	S55539	Ig heavy chain V r
10	462.5	74.1	118	2	PH0097	Ig heavy chain V r
11	462	74.0	118	2	S20641	Ig heavy chain V r
12	461	73.9	117	2	PL0249	Ig heavy chain V r
13	460	73.7	120	2	S55538	Ig heavy chain V r
14	457.5	73.3	254	2	B31790	Ig heavy chain V r
15	456.5	73.2	118	2	PH0096	Ig heavy chain V r
16	456	73.1	119	2	S31107	Ig heavy chain - h
17	456	73.1	124	2	C27888	Ig heavy chain V r
18	456	73.1	138	2	S31666	Ig heavy chain V r
19	455.5	73.0	112	2	S26327	Ig heavy chain V r
20	454	72.8	117	2	PL0252	Ig heavy chain V r
21	452.5	72.5	121	2	A27888	Ig heavy chain V r
22	452.5	72.5	121	2	S55540	Ig heavy chain V r
23	451.5	72.4	121	2	D27888	Ig heavy chain V r
24	451.5	72.4	121	2	B27888	Ig heavy chain V r
25	450.5	72.2	119	2	D27889	Ig heavy chain V r
26	449.5	72.0	113	2	S26468	Ig heavy chain V r
27	449.5	72.0	121	2	H27887	Ig heavy chain V r
28	448.5	71.9	139	2	S38808	Ig heavy chain - m
29	447.5	71.7	548	2	S38864	Ig epsilon chain C
30	447	71.6	152	2	B26471	Ig heavy chain pre
31	446.5	71.6	128	2	S26790	Ig heavy chain V r
32	444.5	71.2	119	2	B27889	Ig heavy chain V r
33	443.5	71.1	121	2	H27888	Ig heavy chain V r
34	443	71.0	119	2	PH0098	Ig heavy chain V r
35	442	70.8	124	2	I27888	Ig heavy chain V r
36	441.5	70.8	108	2	PH1010	Ig heavy chain V r
37	441.5	70.8	118	2	S31105	Ig heavy chain (su
38	441	70.7	119	2	D36005	Ig heavy chain V r
39	440	70.5	125	2	S30531	Ig heavy chain V r
40	439.5	70.4	120	2	S12953	Ig heavy chain V r
41	439.5	70.4	123	2	S63597	Ig heavy chain, V
42	439	70.4	119	2	S31108	Ig heavy chain - h
43	438.5	70.3	123	2	G27888	Ig heavy chain V r
44	438	70.2	140	2	S31686	Ig heavy chain V r
45	437.5	70.1	140	2	S70442	Ig heavy chain pre

ALIGNMENTS

RESULT 1
B34353
anti-peptide Fab' B13I2 heavy chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 23-Jul-1999
C;Accession: B34353
R;Stura, E.A.; Stanfield, R.L.; Fieser, T.M.; Balderas, R.S.; Smith, L.R.; Lerner, R.A.
J. Biol. Chem. 264, 15721-15725, 1989
A;Title: Preliminary crystallographic data and primary sequence for anti-peptide Fab' B
A;Reference number: A34353; MUID:89359424; PMID:2504725
A;Accession: B34353
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-119 <STU>
A;Cross-references: GB:M29252; NID:g195657; PIDN:AAA38388.1; PID:g195658
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.8%; Score 479; DB 2; Length 119;
Best Local Similarity 78.2%; Pred. No. 1.3e-37;
Matches 93; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

```
Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||| |||||||:||||||| ||  ||||||||| ||||||| |||||  |:|
Db          1 EVQLVESGGDLVKPGGSLKLSCAASGFTFSRCAMSWVRQTPEKRLEWVAGISSGGSYTFY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
                 |:||||| ||||||:||| ||| |||||||:|:|:|||     :||| ||||||||||
Db         61 PDTVKGRFIISRDNARNTLSLQMSSLRSEDTAIYYCTRYSSDPFYFDYWGQGTTLTVSS 119
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RESULT 2
S55536
Ig heavy chain V region pe20 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
C;Accession: S55536
R;Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
A;Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies usi
utations in the variable region genes.
A;Reference number: S55528; MUID:95239763; PMID:7536850
A;Accession: S55536
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-120 <BOE>
A;Cross-references: EMBL:X82589; NID:g854304; PIDN:CAA57925.1; PID:g854305
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-97/Domain: immunoglobulin homology <IMM>

Query Match 75.5%; Score 471; DB 2; Length 120;

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  Best Local Similarity   78.3%;  Pred. No. 7.1e-37;
  Matches   94;  Conservative    5;  Mismatches   19;  Indels    2;  Gaps    1;

Qy          2 VTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYYS 61
              | | ||||  |||||||:|||||| || |||||||||| ||||||| ||||| |||
Db          1 VQLQESGGGLVKPGGSLKLSCAASGFTFSTYAMSWVRQTPEKRLEWVATISSGGSYTYYP 60

Qy         62 DSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRV--KLGTYYFDSWGQGTTLTVSS 119
              |||||||||||||||||||| |||||:|||:| |:      |  | ||||||:||||
Db         61 DSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCARLYYDYDPYVMDYWGQGTTVTVSS 120


RESULT 3
I27887
Ig heavy chain V region (H37-45) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C;Accession: I27887
R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A;Title: Structural and functional implications of a restricted antibody response to a d
A;Reference number: A91043; MUID:86300658; PMID:2427335
A;Accession: I27887
A;Molecule type: DNA
A;Residues: 1-121 <CAT>
A;Experimental source: strain Balb/c
A;Note: this sequence was determined from the germline gene
C;Comment: This chain was isolated from a hybridoma protein that binds influenza virus h
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             75.4%;  Score 470.5;  DB 2;  Length 121;
  Best Local Similarity   76.9%;  Pred. No. 8e-37;
  Matches   93;  Conservative    8;  Mismatches   17;  Indels    3;  Gaps    1;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||  ||||||||:||||||| || |||||||||| ||||||| |||||: |||
Db          1 EVMLVESGGGLVKPGGSLKLSCAASGFTFSIYAMSWVRQTPEKRLEWVATISSGGTYTYY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTR---VKLGTYYFDSWGQGTTLTV 117
               |||||||||||||||||||||  |||||:|||:| |   ::|  |  | |||||::||
Db         61 PDSVKGRFTISRDNAKNTLYLQMSRLRSEDTAMYYCAREEGLRLEDYAMDYWGQGTSVTV 120

Qy        118 S 118
              |
Db        121 S 121


RESULT 4
S55537
Ig heavy chain V region pe21 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
C;Accession: S55537
R;Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
A;Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies usin
utations in the variable region genes.
A;Reference number: S55528; MUID:95239763; PMID:7536850
A;Accession: S55537
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-120 <BOE>
A;Cross-references: EMBL:X82590; NID:g854306; PIDN:CAA57926.1; PID:g854307
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-97/Domain: immunoglobulin homology <IMM>

  Query Match             75.2%;  Score 469;  DB 2;  Length 120;
  Best Local Similarity   78.3%;  Pred. No. 1.1e-36;
  Matches   94;  Conservative    5;  Mismatches   19;  Indels    2;  Gaps    1;

Qy          2 VTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYYS 61
              | | ||||  |||||||:|||||| | || |||||||||| ||||||| |||||| |||
Db          1 VQLQESGGGLVKPGGSLKLSCAASRFTFSSYAMSWVRQTPEKRLEWVATISSGGSYTYYP 60

Qy         62 DSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRV--KLGTYYFDSWGQGTTLTVSS 119
              |||||||||||||||||||| |||||:|||:|||:       |  | ||||||:||||
Db         61 DSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCTRLYYDYDPYVMDYWGQGTTVTVSS 120


RESULT 5
E27888
Ig heavy chain V region (H35-C6) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C;Accession: E27888
R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A;Title: Structural and functional implications of a restricted antibody response to a d
A;Reference number: A91043; MUID:86300658; PMID:2427335
A;Accession: E27888
A;Molecule type: DNA
A;Residues: 1-122 <CAT>
A;Experimental source: strain Balb/c
A;Note: this sequence was determined from the germline gene
C;Comment: This chain was isolated from a hybridoma protein that binds influenza virus h
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             75.2%;  Score 469;  DB 2;  Length 122;
  Best Local Similarity   75.4%;  Pred. No. 1.1e-36;
  Matches   92;  Conservative    8;  Mismatches   18;  Indels    4;  Gaps    1;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              :| ||||||  ||||||||:||||||| || | |||||||| |||||| |||||| |||
Db          1 DVKLVESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSYTYY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTR----VKLGTYYFDSWGQGTTLT 116
              |||||||||||||||||||| ||:|||:|||:|||     :   |  | |||||::|
Db         61 PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCTRQGEGYRYDDYAMDYWGQGTSVT 120

Qy        117 VS 118
              ||
Db        121 VS 122


RESULT 6
PH1007
Ig heavy chain V region (clone 163-c1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1007
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1007
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-111 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             74.8%;  Score 467;  DB 2;  Length 111;
  Best Local Similarity   82.0%;  Pred. No. 1.5e-36;
  Matches   91;  Conservative    3;  Mismatches   15;  Indels    2;  Gaps    1;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||  ||||||||:||||||| || |||||||||||||||||||  |||
Db          1 EVKLVESGGGLVKPGGSLKLSCAASGFTFSSYAMSWVRQTPAKRLEWVAYISSGGGSTYY 60
```

```
Qy          61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLG--TYYFDSW 109
               ||||||||||||||||||||||| ||||||:|||:|     |  ||||| |
Db          61 PDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCASHYYGSRTYYFDYW 111
```

RESULT 7
F27888
Ig heavy chain V region (H158-89H4) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C;Accession: F27888
R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A;Title: Structural and functional implications of a restricted antibody response to a d
A;Reference number: A91043; MUID:86300658; PMID:2427335
A;Accession: F27888
A;Molecule type: DNA
A;Residues: 1-119 <CAT>
A;Experimental source: strain Balb/c
A;Note: this sequence was determined from the germline gene
C;Comment: This chain was isolated from a hybridoma protein that binds influenza virus h
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match 74.8%; Score 466.5; DB 2; Length 119;
  Best Local Similarity 76.9%; Pred. No. 1.8e-36;
  Matches 93; Conservative 8; Mismatches 15; Indels 5; Gaps 2;

```
Qy           1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
               :| ||||||  ||||||||:|||||||  || | ||||||||  |||||||  ||||||  |||
Db           1 DVKLVESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSYTYY 60

Qy          61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYY---FDSWGQGTTLTV 117
               |||||||||||||||||||||| ||:|||:|||:| | :  |||    | ||||||::||
Db          61 PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCPRGE--TYYDYAMDYWGQGTSVTV 118

Qy         118 S 118
               |
Db         119 S 119
```

RESULT 8
S09258
Ig heavy chain V region precursor - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 23-Jul-1999
C;Accession: S09258
R;Hamada, H.; Maezawa, K.; Tsuruo, T.
Nucleic Acids Res. 18, 1900, 1990
A;Title: Nucleotide sequences of the variable regions of a mouse monoclonal antibody MRK
A;Reference number: S09258; MUID:90245594; PMID:2110659
A;Accession: S09258
A;Molecule type: DNA
A;Residues: 1-138 <HAM>
A;Cross-references: EMBL:X51719; NID:g53207; PIDN:CAA36012.1; PID:g297545
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

  Query Match 74.4%; Score 464; DB 2; Length 138;
  Best Local Similarity 75.6%; Pred. No. 3.7e-36;
  Matches 90; Conservative 7; Mismatches 22; Indels 0; Gaps 0;

```
Qy           1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
               || ||||||  ||||||||:|||||||  || | ||||||||  |||||||  |||||  |||
Db          20 EVILVESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGGNTYY 79

Qy          61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
               |||||||||||||||| ||||| ||||||:|:|:| |      :| ||||||  :|||:
Db          80 PDSVKGRFTISRDNAKNNLYLQMSSLRSEDTALYYCARYYRYEAWFASWGQGTLVTVSA 138
```

RESULT 9
S55539
Ig heavy chain V region pe24 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
C;Accession: S55539
R;Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
A;Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies usi
utations in the variable region genes.
A;Reference number: S55528; MUID:95239763; PMID:7536850
A;Accession: S55539
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-120 <BOE>
A;Cross-references: EMBL:X82593; NID:g854312; PIDN:CAA57929.1; PID:g854313
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-97/Domain: immunoglobulin homology <IMM>

  Query Match 74.2%; Score 463; DB 2; Length 120;
  Best Local Similarity 76.7%; Pred. No. 3.9e-36;
  Matches 92; Conservative 6; Mismatches 20; Indels 2; Gaps 1;

```
Qy           2 VTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYYS 61
               | | ||||  ||||||||:||||||| || ||||||||||  |||||||  ||| || |||
Db           1 VQLQESGGGLVKPGGSLKLSCAASGFTFSSYAMSWVRQTPEKRLEWVATISSSGSYTYYP 60

Qy          62 DSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRV--KLGTYYFDSWGQGTTLTVSS 119
               ||||||||:|||||||||||| ||||||:|||:| |:      |  | |||||||:||||
Db          61 DSVKGRFTMSRDNAKNTLYLQMSSLRSEDTAMYYCVRLYYDYDPYVMDYWGQGTTVTVSS 120
```

RESULT 10
PH0097
Ig heavy chain V region (anti-cyclosporin B) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 16-Aug-1996
C;Accession: PH0097
R;Schmitter, D.; Poch, O.; Zeder, G.; Heinrich, G.F.; Kocher, H.P.; Quesniaux, V.F.J.;
Mol. Immunol. 27, 1029-1038, 1990
A;Title: Analysis of the structural diversity of monoclonal antibodies to cyclosporine.
A;Reference number: PH0087; MUID:91042649; PMID:2122240
A;Accession: PH0097
A;Molecule type: mRNA
A;Residues: 1-118 <SCH>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;50-66/Region: complementarity-determining 2
F;99-105/Region: complementarity-determining 3

  Query Match 74.1%; Score 462.5; DB 2; Length 118;
  Best Local Similarity 79.0%; Pred. No. 4.3e-36;
  Matches 94; Conservative 4; Mismatches 18; Indels 3; Gaps 1;

```
Qy           1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
               :| ||||||  ||||||||:|||||||  || | ||||||||  |||||||  |||||  |||
Db           1 DVKLVESGGGLVKPGGSLKLSCAASGFTFSSYIMSWVRQTPEKRLEWVATISSGGRYTYY 60

Qy          61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
               |||||||||||||||||||||| ||||||:|||: |         || ||||||||||
Db          61 SDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYST---ASGDSFDYWGQGTTLTVSS 116
```

RESULT 11
S20641
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999

```
C;Accession: S20641
R;Losman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.
submitted to the EMBL Data Library, February 1992
A;Description: Relationships among antinuclear antibodies from autoimmune MRL mice react
A;Reference number: S20639
A;Accession: S20641
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-118 <LOS>
A;Cross-references: EMBL:X65003; NID:g52602; PIDN:CAA46136.1; PID:g52603
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             74.0%;  Score 462;  DB 2;  Length 118;
  Best Local Similarity   75.4%;  Pred. No. 4.8e-36;
  Matches   89;  Conservative    6;  Mismatches   23;  Indels    0;  Gaps    0;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||  ||||||||:||||||| ||:| | ||||||||||||||| |||||  |||
Db          1 EVKLVESGGGLVKPGGSLKLSCAASGFTFSNYIMFWVRQTPAKRLEWVANISSGGGNTYY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVS 118
               |||||||||||||  | ||||| ||||||:|||:| |      |  | |||||::|||
Db         61 PDSVKGRFTISRDNVMNILYLQMSSLRSEDTAMYYCARRAYSNYALDFWGQGTSVTVS 118


RESULT 12
PL0249
Ig heavy chain V region (anti-DNA, 3E12VH) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
C;Accession: PL0249
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A;Reference number: PL0231; MUID:90111618; PMID:2104919
A;Accession: PL0249
A;Molecule type: mRNA
A;Residues: 1-117 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;36-49/Region: framework 2
F;50-66/Region: complementarity-determining 2
F;67-98/Region: framework 3
F;99-108/Region: complementarity-determining 3
F;109-117/Region: framework 4

  Query Match             73.9%;  Score 461;  DB 2;  Length 117;
  Best Local Similarity   75.2%;  Pred. No. 5.9e-36;
  Matches   88;  Conservative    8;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||  ||||||||:|||||||| || | ||||||||||||||| ||  |  |||
Db          1 EVKLVESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPAKRLEWVANISRRGGSTYY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTV 117
               |||||||||||||:||||||| ||||||:|:|:| |      ::|| || |||:||
Db         61 PDSVKGRFTISRDNARNTLYLQMSSLRSEDTAVYYCARRDYSHWFFDVWGAGTTVTV 117


RESULT 13
S55538
Ig heavy chain V region pe22 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
C;Accession: S55538
R;Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
A;Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies usin
utations in the variable region genes.
A;Reference number: S55528; MUID:95239763; PMID:7536850
A;Accession: S55538
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-120 <BOE>
A;Cross-references: EMBL:X82591; NID:g854308; PIDN:CAA57927.1; PID:g854309
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-97/Domain: immunoglobulin homology <IMM>

  Query Match             73.7%;  Score 460;  DB 2;  Length 120;
  Best Local Similarity   75.8%;  Pred. No. 7.5e-36;
  Matches   91;  Conservative    7;  Mismatches   20;  Indels    2;  Gaps    1;

Qy          2 VTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYYS 61
              | | ||||  |||||||:||||||| || |||||||||| ||||||| ||| |: |||
Db          1 VKLQESGGGLVKPGGSLKLSCAASGFTFSSYAMSWVRQTPEKRLEWVATISSSGNYTYYP 60

Qy         62 DSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRV--KLGTYYFDSWGQGTTLTVSS 119
               ||||||||:||||||||||||| ||||||:|||:| |:       |  | |||||||:||||
Db         61 DSVKGRFTMSRDNAKNTLYLQMSSLRSEDTAMYYCVRLYYDYDPYVMDFWGQGTTVTVSS 120


RESULT 14
B31790
Ig heavy chain V region (17/9) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 23-May-1997
C;Accession: B31790
R;Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.
J. Biol. Chem. 263, 17100-17105, 1988
A;Title: Preliminary crystallographic data, primary sequence, and binding data for an an
A;Reference number: A92686; MUID:89034213; PMID:3182835
A;Accession: B31790
A;Molecule type: mRNA
A;Residues: 1-254 <SCH>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             73.3%;  Score 457.5;  DB 2;  Length 254;
  Best Local Similarity   75.8%;  Pred. No. 2.8e-35;
  Matches   91;  Conservative    8;  Mismatches   20;  Indels    1;  Gaps    1;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||| ||||||||:|||||||:|| | |||||||| ||||||| ||:||  |||
Db          1 EVQLVESGGDLVKPGGSLKLSCAASGFSFSSYGMSWVRQTPDKRLEWVATISNGGGYTYY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCT-RVKLGTYYFDSWGQGTTLTVSS 119
               |||||||||||||||||||||| ||:|||||:|  | :     |  |||||  :|||:
Db         61 PDSVKGRFTISRDNAKNTLYLQMSSLKSEDSAMYYCARRERYDENGFAYWGQGTLVTVSA 120


RESULT 15
PH0096
Ig heavy chain V region (anti-cyclosporin A) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 16-Aug-1996
C;Accession: PH0096
R;Schmitter, D.; Poch, O.; Zeder, G.; Heinrich, G.F.; Kocher, H.P.; Quesniaux, V.F.J.; V
Mol. Immunol. 27, 1029-1038, 1990
A;Title: Analysis of the structural diversity of monoclonal antibodies to cyclosporine.
A;Reference number: PH0087; MUID:91042649; PMID:2122240
A;Accession: PH0096
A;Molecule type: mRNA
A;Residues: 1-118 <SCH>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;50-66/Region: complementarity-determining 2
F;99-105/Region: complementarity-determining 3
```

Query Match 73.2%; Score 456.5; DB 2; Length 118;
Best Local Similarity 76.5%; Pred. No. 1.5e-35;
Matches 91; Conservative 10; Mismatches 15; Indels 3; Gaps 2;

```
Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              :| ||||||  ||||||||:||||| | || |:||||||| ||||||| ||||||  |||
Db          1 DVKLVESGGGLVKPGGSLKLSCAASRFTFSSYSMSWVRQTPEKRLEWVATISSGGSYTYY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
               |::|||||||||||||||||| ||:|||:|||:|| |  ||   | ||||::||||
Db         61 PDNMKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCT-VSTGT--MDYWGQGTSVTVSS 116
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Job time : 7.43029 secs

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OM protein - protein search, using sw model

Run on: December 23, 2004, 18:31:20 ; Search time 33.1041 Seconds
(without alignments)
2068.313 Million cell updates/sec

Title: US-10-089-500-55
Perfect score: 624
Sequence: 1 EVTLVESGGDFVKPGGSLKV.....KLGTYYFDSWGQGTTLTVSS 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	469	75.2	255	2	Q6KB05	Q6kb05 mus musculu
2	469	75.2	255	2	CAG34081	Cag34081 mus muscu
3	468.5	75.1	487	2	Q99KA4	Q99ka4 mus musculu
4	463	74.2	119	2	Q920E7	Q920e7 mus musculu
5	455	72.9	486	2	Q91Z07	Q91z07 mus musculu
6	450	72.1	479	2	Q91WP5	Q91wp5 mus musculu
7	439.5	70.4	473	2	Q91Z05	Q91z05 mus musculu
8	438	70.2	128	2	BAD00406	Bad00406 camelus d
9	435	69.7	124	2	BAD00534	Bad00534 camelus d
10	433.5	69.5	125	2	BAD00491	Bad00491 camelus d
11	433	69.4	117	2	AAL35877	Aal35877 lama glam
12	431.5	69.2	606	2	Q6GMY2	Q6gmy2 homo sapien
13	431	69.1	117	1	HV55_MOUSE	P18526 mus musculu
14	430	68.9	121	2	Q9UL71	Q9ul71 homo sapien
15	429	68.8	480	2	Q91XE1	Q91xe1 mus musculu
16	428.5	68.7	471	2	AAH24289	Aah24289 homo sapi
17	427	68.4	119	2	AAL35865	Aal35865 lama glam
18	426	68.3	478	2	Q6PI81	Q6pi81 homo sapien
19	426	68.3	478	2	AAH41037	Aah41037 homo sapi
20	425	68.1	464	2	Q6MZU6	Q6mzu6 homo sapien
21	425	68.1	464	2	CAE45931	Cae45931 homo sapi
22	424.5	68.0	126	2	BAD00225	Bad00225 camelus d
23	424	67.9	126	2	BAD00420	Bad00420 camelus d
24	424	67.9	128	2	BAD00444	Bad00444 camelus d
25	424	67.9	485	2	Q6PDB8	Q6pdb8 mus musculu
26	424	67.9	485	2	AAH58814	Aah58814 mus muscu
27	423.5	67.9	124	2	BAD00233	Bad00233 camelus d
28	423.5	67.9	136	1	HV16_MOUSE	P01783 mus musculu
29	422.5	67.7	127	2	BAD00475	Bad00475 camelus d
30	422	67.6	126	2	BAD00480	Bad00480 camelus d
31	421.5	67.5	129	2	BAD00424	Bad00424 camelus d
32	421	67.5	122	2	BAD00446	Bad00446 camelus d
33	421	67.5	126	2	BAD00510	Bad00510 camelus d
34	419.5	67.2	465	2	Q6P6C4	Q6p6c4 homo sapien
35	419.5	67.2	465	2	AAH62335	Aah62335 homo sapi
36	418.5	67.1	121	2	BAD00459	Bad00459 camelus d
37	418	67.0	123	2	BAD00234	Bad00234 camelus d
38	417.5	66.9	118	2	AAL35882	Aal35882 lama glam
39	417.5	66.9	121	2	BAD00525	Bad00525 camelus d
40	417	66.8	117	1	HV54_MOUSE	P18525 mus musculu
41	417	66.8	470	2	Q6PJA4	Q6pja4 homo sapien
42	417	66.8	470	2	AAH18747	Aah18747 homo sapi
43	416	66.7	117	2	AAL35875	Aal35875 lama glam
44	415.5	66.6	125	2	BAD00439	Bad00439 camelus d
45	415.5	66.6	125	2	BAD00509	Bad00509 camelus d

ALIGNMENTS

RESULT 1
Q6KB05
ID Q6KB05 PRELIMINARY; PRT; 255 AA.
AC Q6KB05;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE ScFv B8E5 protein (Fragment).
GN Name=scFv B8E5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/c;
RA Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,
RA Briand J.P., Hoebeke J.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ746180; CAG34081.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGv; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER 1 1
SQ SEQUENCE 255 AA; 27445 MW; B68BD38395DF713B CRC64;

Query Match 75.2%; Score 469; DB 2; Length 255;
Best Local Similarity 77.0%; Pred. No. 4.3e-41;
Matches 94; Conservative 7; Mismatches 17; Indels 4; Gaps 2;

```
Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              :| | :|||| |||||||||||||||| || | |||||||| ||||||| |:|||| |||
Db          1 QVQLQQSGGDLVKPGGSLKVSCAASGFTFSSYGMSWVRQTPDKRLEWVATITSGGSYTYY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYY---FDSWGQGTTLTV 117
               |||||||||||||||||||| ||:|||:|||:| | :   |   || |||||||||
Db         61 PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCAR-HINYRYDGAFDYWGQGTTLTV 119

Qy        118 SS 119
               ||
Db        120 SS 121
```

RESULT 2
CAG34081
ID CAG34081 PRELIMINARY; PRT; 255 AA.
AC CAG34081;
DT 01-JUN-2004 (TrEMBLrel. 27, Created)
DT 01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DT 01-JUN-2004 (TrEMBLrel. 27, Last annotation update)

```
DE   ScFv B8E5 protein (Fragment).
GN   SCFV B8E5.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=balb/c;
RA   Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,
RA   Briand J.P., Hoebeke J.;
RT   "Modulation of the M2 muscarinic receptor activity with monoclonal
RT   anti-M2 receptor antibody fragments.";
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ746180; CAG34081.1; -.
FT   NON_TER      1      1
SQ   SEQUENCE   255 AA;  27445 MW;  B68BD38395DF713B CRC64;

  Query Match             75.2%;  Score 469;  DB 2;  Length 255;
  Best Local Similarity   77.0%;  Pred. No. 4.3e-41;
  Matches   94;  Conservative    7;  Mismatches   17;  Indels    4;  Gaps    2;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              :| | :|||| |||||||||||||||| || | |||||||| ||||||| |:|||| |||
Db          1 QVQLQQSGGDLVKPGGSLKVSCAASGFTFSSYGMSWVRQTPDKRLEWVATITSGGSYTYY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYY---FDSWGQGTTLTV 117
               |||||||||||||||||||| ||:|||:|||:| |  :   |   || |||||||||
Db         61 PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCAR-HINYRYDGAFDYWGQGTTLTV 119

Qy        118 SS 119
              ||
Db        120 SS 121


RESULT 3
Q99KA4
ID   Q99KA4      PRELIMINARY;      PRT;   487 AA.
AC   Q99KA4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   LOC380791 protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Czech II;
RC   TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Czech II;
RC   TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
RA   Strausberg R.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC004786; AAH04786.1; -.
DR   HSSP; P01810; 2FBJ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 2.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ   SEQUENCE   487 AA;  52554 MW;  7DC8E96DB333077B CRC64;

  Query Match             75.1%;  Score 468.5;  DB 2;  Length 487;
  Best Local Similarity   75.0%;  Pred. No. 1e-40;
  Matches   93;  Conservative    7;  Mismatches   19;  Indels    5;  Gaps    1;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || |||||  ||||||||:||||||| || |||||||||| ||||||| || ||| |||
Db         20 EVQLVESGGGLVKPGGSLKLSCAASGFTFSSYAMSWVRQTPEKRLEWVATISDGGSYTYY 79

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYY-----FDSWGQGTTL 115
               |:|||||||||||| |||||  |:|||:|||:| |   |: |      || ||||||:
Db         80 PDNVKGRFTISRDNAKNNLYLQMSHLKSEDTAMYYCARDMGGSPYGGYSRFDYWGQGTTI 139

Qy        116 TVSS 119
              ||||
Db        140 TVSS 143


RESULT 4
Q920E7
ID   Q920E7      PRELIMINARY;      PRT;   119 AA.
AC   Q920E7;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Pterin-mimicking anti-idiotope heavy chain variable region
DE   (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF307937; AAL09421.1; -.
DR   PIR; C25913; C25913.
DR   HSSP; P01783; 1IGC.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER      1      1
FT   NON_TER    119    119
SQ   SEQUENCE   119 AA;  13025 MW;  F6E904044381CA7C CRC64;

  Query Match             74.2%;  Score 463;  DB 2;  Length 119;
  Best Local Similarity   77.7%;  Pred. No. 7.8e-41;
  Matches   94;  Conservative    6;  Mismatches   17;  Indels    4;  Gaps    2;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||| ||||||||:||||||| || | |||||||| ||||||| |||||| |||
Db          1 EVQLVESGGDLVKPGGSLKLSCAASGFTFSSYGMSWVRQTPDKRLEWVATISSGGSYTYY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTY--YFDSWGQGTTLTVS 118
```

```
Db         61 PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCAR--HGDYDVGFAYWGQGTLVTVS 118

Qy        119 S 119
              :
Db        119 A 119
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RESULT 5
Q91Z07
ID Q91Z07 PRELIMINARY; PRT; 486 AA.
AC Q91Z07;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE LOC380791 protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II;
RC TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II;
RC TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC010324; AAH10324.1; -.
DR HSSP; P01789; 1MCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ SEQUENCE 486 AA; 52681 MW; 4FEF835125DA870B CRC64;

Query Match 72.9%; Score 455; DB 2; Length 486;
Best Local Similarity 71.0%; Pred. No. 2.7e-39;
Matches 88; Conservative 14; Mismatches 16; Indels 6; Gaps 2;

```
Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||  ||||||||:||  |||:|: | |||||||| :|||||| |:|||: |||
Db         20 EVHLVESGGGLVKPGGSLKLSCVVSGFSFTSYDMSWVRQTPERRLEWVAAITSGGN-TYY 78

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTY-----YFDSWGQGTTL 115
               |:||||||:|||||| |||||| ||:|||:|||:| | ::  |     ||||||||||:
Db         79 PDNVKGRFTVSRDNAKYTLYLQMSSLKSEDTAMYYCVRPEIPIYYYSGSYFDSWGQGTTI 138

Qy        116 TVSS 119
              ||||
Db        139 TVSS 142
```

RESULT 6
Q91WP5
ID Q91WP5 PRELIMINARY; PRT; 479 AA.
AC Q91WP5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-VJ558 protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC013656; AAH13656.1; -.
DR HSSP; P01789; 1MCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ SEQUENCE 479 AA; 51603 MW; ECB2D0877748584F CRC64;

Query Match 72.1%; Score 450; DB 2; Length 479;
Best Local Similarity 73.9%; Pred. No. 8.9e-39;
Matches 88; Conservative 9; Mismatches 18; Indels 4; Gaps 1;

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Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||  ||||||||||||||||  ||:||||||||:| |||||||  |:| |  |||
Db         20 EVQLVESGGGLVKPGGSLKVSCAASGLTFSNYAMSWVRQSPEKRLEWVAAINSNGGNTYY 79

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
```

```
                ||::|||||||||||||:|||||| ||||||:| |:| |      ||| || || :||||
Db         80 SDTMKGRFTISRDNAKSTLYLQMSSLRSEDTAFYYCVR----GGYFDVWGAGTAVTVSS 134


RESULT 7
Q91Z05
ID   Q91Z05      PRELIMINARY;      PRT;   473 AA.
AC   Q91Z05;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Expressed sequence AU044919.
GN   Name=AU044919;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CZECH II;
RC   TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RC   Expression driven by an MMTV-LTR enhancer.;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CZECH II;
RC   TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RC   Expression driven by an MMTV-LTR enhancer.;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC010327; AAH10327.1; -.
DR   PIR; S68213; S68213.
DR   HSSP; P01783; 1IGC.
DR   MGD; MGI:2144967; AU044919.
DR   InterPro; IPR000345; CytC_heme_BS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   473 AA;  51946 MW;  CF625F008932AF12 CRC64;

  Query Match             70.4%;  Score 439.5;  DB 2;  Length 473;
  Best Local Similarity   72.3%;  Pred. No. 1.1e-37;
  Matches   86;  Conservative   10;  Mismatches   22;  Indels    1;  Gaps    1;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||  |||||| |:||||||| || | | |||| | | |||||||:|| :  ||

Db         20 EVQLVESGGGLVKPGGSRKLSCAASGFTFSDYGMHWVRQAPEKGLEWVAYINSGSTTIYY 79

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
              :|:|||||||||||||:||| ||||||:|||:| | :|     | ||||||:||||
Db         80 ADTVKGRFTISRDNAKNTLFLQMTSLRSEDTAMYYCAR-ELWLRRIDYWGQGTTITVSS 137


RESULT 8
BAD00406
ID   BAD00406    PRELIMINARY;      PRT;   128 AA.
AC   BAD00406;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Immunoglobulin heavy chain VHDJ region (Fragment).
GN   IGVH.
OS   Camelus dromedarius (Dromedary) (Arabian camel).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX   NCBI_TaxID=9838;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Honda T., Akahori Y., Kurosawa Y.;
RT   "Libraries of heavy-chain antibodies reflecting camel gamma2 and
RT   gamma3 in vivo repertoires.";
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB092044; BAD00406.1; -.
FT   NON_TER       1      1
FT   NON_TER     128    128
SQ   SEQUENCE   128 AA;  13856 MW;  7C23CF09C28B8B9A CRC64;

  Query Match             70.2%;  Score 438;  DB 2;  Length 128;
  Best Local Similarity   65.6%;  Pred. No. 3.6e-38;
  Matches   82;  Conservative   17;  Mismatches   20;  Indels    6;  Gaps    1;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||  |:|||||::||||||| || |||:|||| | | ||||: |:|||  |||
Db          1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSAINSGGGSTYY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKL------GTYYFDSWGQGTT 114
              :|||||||||||||||||||: ||::||:|||:| : :       | |  | ||:||
Db         61 ADSVKGRFTISRDNAKNTLYLQLNSLKTEDTAMYYCAKDRYGGRWLSGDYSMDYWGKGTL 120

Qy        115 LTVSS 119
              :|:||
Db        121 VTISS 125


RESULT 9
BAD00534
ID   BAD00534    PRELIMINARY;      PRT;   124 AA.
AC   BAD00534;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Immunoglobulin heavy chain VHDJ region (Fragment).
GN   IGVH.
OS   Camelus dromedarius (Dromedary) (Arabian camel).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX   NCBI_TaxID=9838;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Honda T., Akahori Y., Kurosawa Y.;
RT   "Libraries of heavy-chain antibodies reflecting camel gamma2 and
RT   gamma3 in vivo repertoires.";
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB092172; BAD00534.1; -.
FT   NON_TER       1      1
FT   NON_TER     124    124
SQ   SEQUENCE   124 AA;  13421 MW;  B31996777375A27E CRC64;
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  Query Match             69.7%;  Score 435;  DB 2;  Length 124;
  Best Local Similarity   66.9%;  Pred. No. 7.3e-38;
  Matches   81;  Conservative   17;  Mismatches   21;  Indels    2;  Gaps    1;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              :| ||||||  |:|||||::|||||| || |||:|||| | | ||||: | | |  |||
Db          1 QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTIKSAGGSTYY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDS--WGQGTTLTVS 118
              :|||||||||||||||||||: ||::||:|||:|  :: |::|     ||||| :|||
Db         61 ADSVKGRFTISRDNAKNTLYLQLNSLKTEDTAMYYCANLEFGSWYSPRGYWGQGTQVTVS 120

Qy        119 S 119
              |
Db        121 S 121


RESULT 10
BAD00491
ID   BAD00491    PRELIMINARY;      PRT;   125 AA.
AC   BAD00491;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Immunoglobulin heavy chain VHDJ region (Fragment).
GN   IGVH.
OS   Camelus dromedarius (Dromedary) (Arabian camel).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX   NCBI_TaxID=9838;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Honda T., Akahori Y., Kurosawa Y.;
RT   "Libraries of heavy-chain antibodies reflecting camel gamma2 and
RT   gamma3 in vivo repertoires.";
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB092129; BAD00491.1; -.
FT   NON_TER       1      1
FT   NON_TER     125    125
SQ   SEQUENCE   125 AA;  13593 MW;  F1637892B028E48C CRC64;

  Query Match             69.5%;  Score 433.5;  DB 2;  Length 125;
  Best Local Similarity   67.2%;  Pred. No. 1.1e-37;
  Matches   82;  Conservative   18;  Mismatches   19;  Indels    3;  Gaps    1;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||  |:|||||::|||||| ||:|:|||||| | | ||||| |:|||: |||
Db          1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSNYSMSWVRQAPGKGLEWVAAINSGGTSTYY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYY---FDSWGQGTTLTV 117
              ::||||||||||||||||:|  ||::||:|||:| :    : |    | :|||||  :||
Db         61 TESVKGRFTISRDNAKNTLYVQFNSLKTEDTAMYYCAKGHYNSDYDRTFANWGQGTHVTV 120

Qy        118 SS 119
              ||
Db        121 SS 122


RESULT 11
AAL35877
ID   AAL35877    PRELIMINARY;      PRT;   117 AA.
AC   AAL35877;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Immunoglobulin heavy chain variable domain (Fragment).
OS   Lama glama (Llama).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
OX   NCBI_TaxID=9844;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22007448; PubMed=12009207;
RA   Tanha J., Dubuc G., Hirama T., Narang S.A., MacKenzie C.R.;
RT   "Selection by phage display of llama conventional V(H) fragments with
RT   heavy chain antibody V(H)H properties.";
RL   J. Immunol. Methods 263:97-109(2002).
DR   EMBL; AF442946; AAL35877.1; -.
FT   NON_TER       1      1
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  12459 MW;  08F5E4BA402F98D1 CRC64;

  Query Match             69.4%;  Score 433;  DB 2;  Length 117;
  Best Local Similarity   68.9%;  Pred. No. 1.1e-37;
  Matches   82;  Conservative   15;  Mismatches   20;  Indels    2;  Gaps    1;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || |  |||  |:|||||::|||||| || |||||||| | | ||||: |:|||  |||
Db          1 EVQLQASGGGLVQPGGSLRLSCAASGFTFSGYAMSWVRQAPGKGLEWVSSINSGGGSTYY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
              :|||||||||||||||||:||| ||: ||:|:|:| | : |::  | |||||  :||||
Db         61 ADSVKGRFTISRDNAKNTLFLQMNSLKPEDTALYYCARTQTGSH--DYWGQGTQVTVSS 117


RESULT 12
Q6GMY2
ID   Q6GMY2      PRELIMINARY;      PRT;   606 AA.
AC   Q6GMY2;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073758; AAH73758.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 4.
DR   Pfam; PF00047; ig; 4.
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DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW   Hypothetical protein.
SQ   SEQUENCE   606 AA;  66184 MW;  B6B38B51114E4C55 CRC64;

  Query Match             69.2%;  Score 431.5;  DB 2;  Length 606;
  Best Local Similarity   64.2%;  Pred. No. 1e-36;
  Matches   86;  Conservative   13;  Mismatches   20;  Indels   15;  Gaps    2;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              :| ||||||  |||||||::|||||||  || | |||:|| | | ||||:||||  | | |
Db         20 QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSSSYTNY 79

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTR----------VKLGTYYF--- 106
              :||||||||||||||:||||| |||:||:|:|:|:| |          |    ||:
Db         80 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARGGNGIAAAGRVVYAEDYYYYYG 139

Qy        107 -DSWGQGTTLTVSS 119
               | ||||||:||||
Db        140 MDVWGQGTTVTVSS 153


RESULT 13
HV55_MOUSE
ID   HV55_MOUSE     STANDARD;      PRT;   117 AA.
AC   P18526;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig heavy chain V region 345 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/cJ;
RX   MEDLINE=89279149; PubMed=2499654;
RA   Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT   "Early onset of somatic mutation in immunoglobulin VH genes during the
RT   primary immune response.";
RL   J. Exp. Med. 169:2007-2019(1989).
CC   -!- MISCELLANEOUS: This sequence belongs to the VH7183 subfamily.
DR   PIR; JT0502; HVMS34.
DR   HSSP; P01783; 1IGC.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    117       Ig heavy chain V region 345.
FT   DOMAIN       20     49       Framework-1.
FT   DOMAIN       50     54       Complementarity-determining-1.
FT   DOMAIN       55     68       Framework-2.
FT   DOMAIN       69     85       Complementarity-determining-2.
FT   DOMAIN       86    117       Framework-3.
FT   DISULFID     41    115       By similarity.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  12902 MW;  49380E4627ACA99A CRC64;

  Query Match             69.1%;  Score 431;  DB 1;  Length 117;
  Best Local Similarity   83.7%;  Pred. No. 1.8e-37;
  Matches   82;  Conservative    5;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||  ||||||||:|||||||||| | |||||||| ||||||||||||  ||| 
Db         20 EVQLVESGGGLVKPGGSLKLSCAASGFAFSSYDMSWVRQTPEKRLEWVAYISSGGGSTYY 79

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTR 98
              |:||||||||||||||||||| ||:|||:|||:| |
Db         80 PDTVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCAR 117


RESULT 14
Q9UL71
ID   Q9UL71      PRELIMINARY;      PRT;   121 AA.
AC   Q9UL71;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035043; AAD56279.1; -.
DR   HSSP; P01852; 1NFD.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     121    121
SQ   SEQUENCE   121 AA;  13154 MW;  2F045CCFA5D50736 CRC64;

  Query Match             68.9%;  Score 430;  DB 2;  Length 121;
  Best Local Similarity   67.8%;  Pred. No. 2.4e-37;
  Matches   82;  Conservative   14;  Mismatches   23;  Indels    2;  Gaps    1;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||  |:|||||:: |||||| |  ||| |||| | | ||||: ||  |  |||
Db          1 EVQLVESGGGVVQPGGSLRLFCAASGFTFDGYAMHWVRQAPGKGLEWVSLISGDGGSTYY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYY--FDSWGQGTTLTVS 118
              :|||||||||||||:||:||||| |||:||:|:|:|: : |: | |  || ||||| :|||
Db         61 ADSVKGRFTISRDNSKNSLYLQMNSLRAEDTALYYCAKGKVTTIYDRFDIWGQGTMVTVS 120

Qy        119 S 119
               |
Db        121 S 121


RESULT 15
Q91XE1
ID   Q91XE1      PRELIMINARY;      PRT;   480 AA.
AC   Q91XE1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Igh-VJ558 protein (Fragment).
GN   Name=Igh-VJ558;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Colon;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Colon;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC010798; AAH10798.1; -.
DR   HSSP; P01789; 1MCP.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 2.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
FT   NON_TER       1       1
SQ   SEQUENCE   480 AA;  51936 MW;  20B9234EEF2B41ED CRC64;

  Query Match             68.8%;  Score 429;  DB 2;  Length 480;
  Best Local Similarity   70.8%;  Pred. No. 1.5e-36;
  Matches   85;  Conservative   13;  Mismatches   18;  Indels    4;  Gaps    2;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              :| ||||||  |||||||::|||||||  ||:  |||||||| |||||||  ||: |  |:|
Db         19 DVKLVESGGGLVKPGGSLRLSCAASGFIFSNSYMSWVRQTPEKRLEWVATISNSGYATHY 78

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTY-YFDSWGQGTTLTVSS 119
               ||:||||||||||:||: ||| || |||:|:|:|||   | | ||| || |||:||||
Db         79 PDSMKGRFTISRDNAQNTVLLQMTSLNSEDTAVYYCTR---GDYWYFDVWGAGTTVTVSS 135


Search completed: December 23, 2004, 19:04:39
Job time : 34.1041 secs
```

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2004, 18:30:04 ; Search time 28.8913 Seconds
(without alignments)
1340.986 Million cell updates/sec

Title: US-10-089-500-56
Perfect score: 572
Sequence: 1 DIQMTQTASSLPASLGDRVT.....HQYSKLPWTFGGGTKLEIKR 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	572	100.0	108	4	AAB81990	Aab81990 Gangliosi
2	572	100.0	108	6	ABU11013	Abu11013 Modified
3	572	100.0	128	3	AAB01628	Aab01628 Murine im
4	572	100.0	128	4	AAB81978	Aab81978 Gangliosi
5	572	100.0	128	6	ABU11003	Abu11003 Modified
6	564	98.6	128	2	AAY28368	Aay28368 pKM641 LA
7	562	98.3	128	2	AAR33257	Aar33257 Rat immun
8	557	97.4	128	2	AAR53340	Aar53340 KM641 H c
9	521	91.1	108	2	AAW00834	Aaw00834 Variable
10	520	90.9	127	2	AAR12359	Aar12359 Light (ka
11	516	90.2	108	2	AAW04177	Aaw04177 Variant v
12	516	90.2	108	2	AAW16620	Aaw16620 Anti-huma
13	516	90.2	128	4	AAB81998	Aab81998 Gangliosi
14	516	90.2	650	6	ABR62591	Abr62591 Anti-CD7
15	516	90.2	651	6	ABR62590	Abr62590 Anti-CD7
16	515	90.0	126	2	AAR12237	Aar12237 Mouse MAb
17	514	89.9	108	4	AAB81988	Aab81988 Gangliosi
18	514	89.9	128	4	AAB81999	Aab81999 Gangliosi
19	511	89.3	128	4	AAB81992	Aab81992 Gangliosi
20	510	89.2	108	2	AAW70620	Aaw70620 Anti-VEGF
21	510	89.2	108	5	ABP61189	Abp61189 Murine an
22	508	88.8	108	6	ABU11011	Abu11011 Modified
23	507	88.6	128	4	AAB81994	Aab81994 Gangliosi
24	507	88.6	214	8	ADN41870	Adn41870 Amino aci
25	506	88.5	128	4	AAB81995	Aab81995 Gangliosi
26	502	87.8	131	2	AAR84553	Aar84553 MAb SCH94
27	501	87.6	128	4	AAB81997	Aab81997 Gangliosi
28	500	87.4	131	8	ADI26634	Adi26634 Human ant
29	499	87.2	128	4	AAB81996	Aab81996 Gangliosi
30	498	87.1	112	4	AAE00697	Aae00697 Human imm
31	497	86.9	109	4	AAB62050	Aab62050 Mouse mon
32	497	86.9	109	6	ABP72768	Abp72768 Anti-full
33	497	86.9	128	4	AAB81993	Aab81993 Gangliosi
34	495	86.5	119	8	ADM78045	Adm78045 Human SKB
35	494	86.4	108	4	AAB81986	Aab81986 Gangliosi
36	491	85.8	107	6	ABJ18571	Abj18571 Gangliosi
37	491	85.8	107	6	ABJ18574	Abj18574 Gangliosi
38	490	85.7	107	2	AAW66098	Aaw66098 anti-CD22
39	490	85.7	107	6	AAO27199	Aao27199 Murine an
40	490	85.7	107	7	ADC84579	Adc84579 CDR3 heav
41	490	85.7	107	8	ADH50840	Adh50840 Mouse ant
42	490	85.7	109	8	ADG25821	Adg25821 Anti-CD30
43	488	85.3	107	2	AAW49812	Aaw49812 Amino aci
44	488	85.3	107	6	ABR55867	Abr55867 Anti-glyc
45	488	85.3	107	8	ADN49724	Adn49724 Variable

ALIGNMENTS

RESULT 1
AAB81990
ID AAB81990 standard; protein; 108 AA.
XX
AC AAB81990;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 56.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
XX
OS Mus musculus.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Claim 11; Page 174-175; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 108 AA;

Query Match 100.0%; Score 572; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.3e-39;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
```

RESULT 2
ABU11013
ID ABU11013 standard; protein; 108 AA.
XX
AC ABU11013;
XX
DT 04-FEB-2003 (first entry)
XX
DE Modified ganglioside GD3 antibody associated protein #6.
XX
KW Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
XX
OS Mus musculus.
XX
PN WO200278739-A1.
XX
PD 10-OCT-2002.
XX
PF 29-MAR-2002; 2002WO-JP003170.
XX
PR 29-MAR-2001; 2001JP-00097483.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Shitara K, Niwa R, Kanazawa J, Asada M;
XX
DR WPI; 2003-067410/06.
XX
PT Drugs containing genetically-modified antibody against ganglioside GD3,
PT its fragment, immunocompetent cell activators or/and antitumor agents in
PT combination, applicable in treating malignant tumor like melanoma.
XX
PS Claim 7; Page 113; 121pp; Japanese.
XX
CC The invention describes drugs contain a genetically-modified antibody
CC against ganglioside GD3 or its fragment and at least 1 of a substance
CC capable of activating immunocompetent cells and a substance having an
CC antitumor activity in combination. The drugs can be used to treat tumour
CC like melanoma and can provide a treatment with enhanced therapeutic
CC effect and little side-reactions, particularly to relieve problems of
CC side-effects during the conventional single administration. This sequence
CC represents a protein associated with the anti- ganglioside GD3 antibody
XX
SQ Sequence 108 AA;

```
  Query Match             100.0%;  Score 572;  DB 6;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-39;
  Matches  108;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
```

RESULT 3
AAB01628
ID AAB01628 standard; protein; 128 AA.
XX
AC AAB01628;
XX
DT 07-DEC-2000 (first entry)
XX
DE Murine immunoglobulin light chain variable region.
XX
KW Mouse; immunoglobulin; L chain; light chain; variable region; cancer;
KW humanised antibody.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Peptide 1. .20
FT /label= signal_peptide
FT Protein 21. .128
FT /label= mature_immunoglobulin_light_chain_V_region
XX
PN EP1013761-A2.
XX
PD 28-JUN-2000.
XX
PF 18-SEP-1992; 99EP-00124345.
XX
PR 18-SEP-1991; 91JP-00238375.
PR 18-SEP-1992; 92EP-00116026.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Shitara K, Hanai N, Hasegawa M, Miyaji H, Kuwana Y;
XX
DR WPI; 2000-402204/35.
DR N-PSDB; AAA51004.
XX
PT New humanized chimera antibody KM-871 useful for treating cancer,
PT comprises variable region of mouse monoclonal antibody, reactive with
PT ganglioside and human antibody constant region.
XX
PS Claim 14; Page 28-29; 65pp; English.
XX
CC The present sequence is a murine immunoglobulin light chain variable
CC region from plasmid KM-641. The coding sequence was used in the creation
CC of an expression vector, along with the sequence for a human antibody, to
CC produce humanised chimaeric antibodies, which can be used to treat
CC cancer. Humanised chimaeric antibodies are more effective than mouse
CC antibodies as they do not provoke a reaction in the human and side
CC effects, such as the formation of anti-mouse immunoglobulin antibody and
CC the rapid half-life of the immunoglobulins, do not occur
XX
SQ Sequence 128 AA;

```
  Query Match             100.0%;  Score 572;  DB 3;  Length 128;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-39;
  Matches  108;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 80

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 128
```

RESULT 4
AAB81978
ID AAB81978 standard; protein; 128 AA.
XX
AC AAB81978;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 2.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;

KW cancer.
XX
OS Mus musculus.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Example 1; Page 140; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 128 AA;

Query Match 100.0%; Score 572; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 3.9e-39;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 21 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 80

Qy 61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 81 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 128

RESULT 5
ABU11003
ID ABU11003 standard; protein; 128 AA.
XX
AC ABU11003;
XX
DT 04-FEB-2003 (first entry)
XX
DE Modified ganglioside GD3 antibody associated protein #2.
XX
KW Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
XX
OS Mus musculus.
XX
PN WO200278739-A1.
XX
PD 10-OCT-2002.
XX
PF 29-MAR-2002; 2002WO-JP003170.
XX
PR 29-MAR-2001; 2001JP-00097483.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Shitara K, Niwa R, Kanazawa J, Asada M;
XX
DR WPI; 2003-067410/06.
XX
PT Drugs containing genetically-modified antibody against ganglioside GD3,
PT its fragment, immunocompetent cell activators or/and antitumor agents in
PT combination, applicable in treating malignant tumor like melanoma.
XX
PS Example 3; Page 98; 121pp; Japanese.
XX
CC The invention describes drugs contain a genetically-modified antibody
CC against ganglioside GD3 or its fragment and at least 1 of a substance
CC capable of activating immunocompetent cells and a substance having an
CC antitumor activity in combination. The drugs can be used to treat tumour
CC like melanoma and can provide a treatment with enhanced therapeutic
CC effect and little side-reactions, particularly to relieve problems of
CC side-effects during the conventional single administration. This sequence
CC represents a protein associated with the anti- ganglioside GD3 antibody
XX
SQ Sequence 128 AA;

Query Match 100.0%; Score 572; DB 6; Length 128;
Best Local Similarity 100.0%; Pred. No. 3.9e-39;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 21 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 80

Qy 61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 81 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 128

RESULT 6
AAY28368
ID AAY28368 standard; protein; 128 AA.
XX
AC AAY28368;
XX
DT 04-NOV-1999 (first entry)
XX
DE pKM641 LA2 immunoglobulin light chain.
XX
KW antibody; nucleotide; genomic; hypervariable region; chimeric;
KW light chain; amino acid.
XX
OS Mus sp.
XX
PN US5939532-A.
XX
PD 17-AUG-1999.
XX
PF 07-JUN-1995; 95US-00483528.
XX
PR 07-SEP-1993; 93US-00116778.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Nakamura K, Hanai N, Kuwana Y, Hasegawa M, Koike M, Shitara K;
XX
DR WPI; 1999-468416/39.
DR N-PSDB; AAX99481.
XX
PT Chimeric human antibody expression vectors.
XX
PS Example 1; Col 99; 188pp; English.
XX
CC This immunoglobulin region was isolated from pKM641LA2.A methionine
CC codon, presumably the initiation codon ATG, was found in the vicinity of
CC the 5' terminus and the sequence has a full length leader sequence. The
CC chimeric human antibodies are useful in the treatment of cancer,
CC especially that which is of neural ectodermal origin. In contrast to
CC prior art constructs based on mouse monoclonal antibodies, the chimeric
CC human antibodies do not cause anti-mouse immunoglobulin production. The

```
CC   chimeric human antibodies have a prolonged half-life and a reduced
CC   frequency of adverse effects when compared to mouse monoclonal antibodies
XX
SQ   Sequence 128 AA;

  Query Match             98.6%;  Score 564;  DB 2;  Length 128;
  Best Local Similarity   99.1%;  Pred. No. 1.7e-38;
  Matches  107;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 80

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              |||||||||||||||||||||||||||||||| ||||||||||
Db         81 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTSGGGTKLEIKR 128


RESULT 7
AAR33257
ID   AAR33257 standard; protein; 128 AA.
XX
AC   AAR33257;
XX
DT   25-MAR-2003  (revised)
DT   12-JUL-1993  (first entry)
XX
DE   Rat immunoglobulin L chain varible region of pKM641LA2.
XX
KW   Promoter; variable; region; rat; immunoglobulin; heavy; H; chain;
KW   humanised; chimeric; antibody; expression vector.
XX
OS   Rattus rattus.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .20
FT                   /note= "Signal peptide"
FT   Protein         21. .128
FT                   /note= "Mature protein"
XX
PN   EP533199-A2.
XX
PD   24-MAR-1993.
XX
PF   18-SEP-1992;   92EP-00116026.
XX
PR   18-SEP-1991;   91JP-00238375.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO CO LTD.
XX
PI   Shitara K,  Hanai N,  Hasegawa M,  Miyaji H,  Kuwana Y;
XX
DR   WPI; 1993-095510/12.
DR   N-PSDB; AAQ33258.
XX
PT   Humanised chimeric antibody prodn. against ganglioside GD3 - for treating
PT   cancers, such as melanoma, neuroblastoma, etc.
XX
PS   Claim 6; Page 30-31; 63pp; English.
XX
CC   The sequences given in AAR33256-57 represent rat heavy and light chain
CC   variable regions respectively. The DNA sequences encoding these proteins
CC   were used in the construction of humanised chimeric antibody expression
CC   vectors. In these humanised antibodies none of the amino acids of the non
CC   -human animal Ab variable region have been changed. (Updated on 25-MAR-
CC   2003 to correct PN field.)
XX
SQ   Sequence 128 AA;

  Query Match             98.3%;  Score 562;  DB 2;  Length 128;
  Best Local Similarity   99.1%;  Pred. No. 2.5e-38;
  Matches  107;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 DIQMTQTASSLLASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 80

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 128


RESULT 8
AAR53340
ID   AAR53340 standard; protein; 128 AA.
XX
AC   AAR53340;
XX
DT   18-NOV-1994  (first entry)
XX
DE   KM641 H chain variable region.
XX
KW   Monoclonal antibody; Ab; ganglioside GM2; chimera; chimeric antibody;
KW   expression vector; heavy; light; chain; hypervariable region; CDR;
KW   constant region; hybridoma; Ig; immunoglobulin; promoter; enhancer.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .20
FT                   /label= sig_peptide
XX
PN   AU9346181-A.
XX
PD   17-MAR-1994.
XX
PF   07-SEP-1993;   93AU-00046181.
XX
PR   07-SEP-1992;   92JP-00238452.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Nakamura K,  Koike M,  Shitara K,  Hanai N,  Kuwana Y,  Hasegawa M;
XX
DR   WPI; 1994-126857/16.
DR   N-PSDB; AAQ45438.
XX
PT   Humanised antibody specific for ganglioside GM2 - used for producing a
PT   cytocidal effect on cancers such as melanoma, neuroblastoma and glioma.
XX
PS   Example 2; Page 115-116; 191pp; English.
XX
CC   Example 2 describes the construction of the vector pChi641HA1 for
CC   chimeric human antibody H chain expression. mRNA from mouse anti-GD3
CC   monoclonal Ab KM641-producing cells was isolated and KM641 H and L chain
CC   cDNAs isolated. The base sequences of the Ig variable regions in KM641 H
CC   chain cDNA (pKM641HA3) and KM641 L chain cDNA (pKM641LA2) are given in
CC   AAQ45438-39. A KM641-derived chimeric human Ab H chain expression vector
CC   was constructed by joining the H chain variable region gene from
CC   pKM641HA3 to a vector for chimeric human Ab H chain expression using the
CC   synthetic DNAs given in AAQ63439 and AAQ63440
XX
SQ   Sequence 128 AA;

  Query Match             97.4%;  Score 557;  DB 2;  Length 128;
  Best Local Similarity   98.1%;  Pred. No. 6.5e-38;
  Matches  106;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 80

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              |||||||||||||||||| |||||||||||||||| ||||||||||
Db         81 RFSGGGSGTDYSLTISNLEPGDIATYFCHQYSKLPWTSGGGTKLEIKR 128
```

```
RESULT 9
AAW00834
ID   AAW00834 standard; protein; 108 AA.
XX
AC   AAW00834;
XX
DT   20-MAY-1997  (first entry)
XX
DE   Variable light chain of anti-human Fas ligand antibody NOK-1.
XX
KW   Variable region; light chain; human; Fas ligand; monoclonal; antibody;
KW   NOK-1; hybridoma; inhibition; apoptosis; assay; diagnosis; disease;
KW   hepatitis; infectious mononucleosis; systemic lupus erythematosus.
XX
OS   Mus musculus.
XX
PN   WO9629350-A1.
XX
PD   26-SEP-1996.
XX
PF   21-MAR-1996;   96WO-JP000734.
XX
PR   20-MAR-1995;   95JP-00087420.
PR   27-OCT-1995;   95JP-00303492.
XX
PA   (SUME ) SUMITOMO ELECTRIC IND CO.
XX
PI   Kayagaki N,  Yagita H,  Okumura K,  Nakata M;
XX
DR   WPI; 1996-443140/44.
DR   N-PSDB; AAT39560.
XX
PT   Monoclonal antibody specifically recognising the Fas ligand - useful for
PT   the detection of Fas ligands either on cell surface or in solution.
XX
PS   Claim 41; Page 93-94; 133pp; Japanese.
XX
CC   The present sequence is the light chain variable region of the anti-human
CC   Fas ligand monoclonal antibody (MAb) NOK-1. NOK-1 is produced by the
CC   hybridoma NOK-1 (FERM BP-5044), which was prepared by immunising mice
CC   with transformed human Fas ligand expressing COS cells, and fusing spleen
CC   cells isolated from the mice with myeloma P3x63Ag8.653 (ATCC CRL-1580)
CC   cells. The MAb recognises the human Fas ligand on the cell surface or in
CC   solution, and can be used to inhibit the apoptosis inducing cell surface
CC   Fas ligand/Fas reaction. The MAb can also be used for a Fas ligand assay
CC   in biological samples (e.g. human blood), especially for disease
CC   diagnosis, e.g. hepatitis, infectious mononucleosis and systemic lupus
CC   erythematosus
XX
SQ   Sequence 108 AA;

  Query Match             91.1%;  Score 521;  DB 2;  Length 108;
  Best Local Similarity   90.7%;  Pred. No. 4.7e-35;
  Matches   98;  Conservative    3;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||| ||| |||||||||| |||||||||||||||||||||:|:| |||||||
Db          1 DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 60

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              |||| |||||||||||||||||||| |||: ||||||||||||
Db         61 RFSGSGSGTDYSLTISNLEPEDIATYFCQQYSEFPWTFGGGTKLEIKR 108


RESULT 10
AAR12359
ID   AAR12359 standard; protein; 127 AA.
XX
AC   AAR12359;
XX
DT   25-MAR-2003  (revised)
DT   15-AUG-1991  (first entry)
XX
DE   Light (kappa) chain variable region of murine 1C11 immunoglobulin.
XX
KW   Chimeric antibodies; immunoconjugates; HIV; AIDS.
XX
OS   Mus musculus.
XX
PN   WO9107493-A.
XX
PD   30-MAY-1991.
XX
PF   13-NOV-1989;   89US-00433730.
XX
PR   13-NOV-1989;   89US-00433730.
XX
PA   (XOMA ) XOMA CORP.
PA   (GREC ) GREEN CROSS CORP.
XX
PI   Better MD,  Horwitz AH,  Ghoshdasti P,  Robinson R;
XX
DR   WPI; 1991-178105/24.
DR   N-PSDB; AAQ12061.
XX
PT   New chimeric mouse-human antibodies - used to detect, kill and remove HIV
PT   -1 antigen from sample.
XX
PS   Disclosure; Fig 13; 107pp; English.
XX
CC   This is the light (kappa)- chain variable (V) region of a mouse
CC   monoclonal antibody (MAb), 1C11, and is specific for an HIV-1 viral
CC   antigen. It is used in the construction of a chimeric MAb comprising
CC   heavy and light chains having murine V regions and human C regions. The
CC   chimeric MAbs are more effective than murine MAb 1C11 since they have an
CC   increased compatibility in humans. The heavy and light chain V-regions
CC   are joined by manipulating their respective joining (J) regions, to
CC   generate restriction enzyme recognition sites. The chimeric MAbs can be
CC   used as immunoconjugates, in association with e.g. toxins for HIV
CC   treatment. They can also be used in diagnosis of HIV. See also AAQ12056-
CC   60 and AAQ12062-63. (Updated on 25-MAR-2003 to correct PA field.)
CC   (Updated on 25-MAR-2003 to correct PI field.) (Updated on 25-MAR-2003 to
CC   correct DR field.)
XX
SQ   Sequence 127 AA;

  Query Match             90.9%;  Score 520;  DB 2;  Length 127;
  Best Local Similarity   91.6%;  Pred. No. 6.6e-35;
  Matches   98;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||| ||| |||||||||||||| |||||||||||||||||||:|:|:|||||||
Db         21 DIQMTQTTSSLSASLGDRVTISCSASQGISNYLNWYQQKPDGTVKLLIYYTSSLHSGVPS 80

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIK 107
              |||| |||||||||||||||||||:| ||||||||||||||||||
Db         81 RFSGSGSGTDYSLTISNLEPEDIATYYCQQYSKLPWTFGGGTKLEIK 127


RESULT 11
AAW04177
ID   AAW04177 standard; protein; 108 AA.
XX
AC   AAW04177;
XX
DT   19-MAY-1997  (first entry)
XX
DE   Variant variable light chain of Fas ligand antibody NOK-1.
XX
KW   Variable region; light chain; human; Fas ligand; monoclonal; antibody;
KW   NOK-1; hybridoma; inhibition; apoptosis; assay; diagnosis; disease;
KW   hepatitis; infectious mononucleosis; systemic lupus erythematosus;
KW   variant.
XX
OS   Mus musculus.
```

XX
PN WO9629350-A1.
XX
PD 26-SEP-1996.
XX
PF 21-MAR-1996; 96WO-JP000734.
XX
PR 20-MAR-1995; 95JP-00087420.
PR 27-OCT-1995; 95JP-00303492.
XX
PA (SUME) SUMITOMO ELECTRIC IND CO.
XX
PI Kayagaki N, Yagita H, Okumura K, Nakata M;
XX
DR WPI; 1996-443140/44.
DR N-PSDB; AAT39550.
XX
PT Monoclonal antibody specifically recognising the Fas ligand - useful for
PT the detection of Fas ligands either on cell surface or in solution.
XX
PS Claim 20; Page 80-81; 133pp; Japanese.
XX
CC The present sequence is a variant light chain variable region of the anti
CC -human Fas ligand monoclonal antibody (MAb) NOK-1. NOK-1 is produced by
CC the hybridoma NOK-1 (FERM BP-5044), which was prepared by immunising mice
CC with transformed human Fas ligand expressing COS cells, and fusing spleen
CC cells isolated from the mice with myeloma P3x63Ag8.653 (ATCC CRL-1580)
CC cells. The MAb recognises the human Fas ligand on the cell surface or in
CC solution, and can be used to inhibit the apoptosis inducing cell surface
CC Fas ligand/Fas reaction. The MAb can also be used for a Fas ligand assay
CC in biological samples (e.g. human blood), especially for disease
CC diagnosis, e.g. hepatitis, infectious mononucleosis and systemic lupus
CC erythematosus
XX
SQ Sequence 108 AA;

Query Match 90.2%; Score 516; DB 2; Length 108;
Best Local Similarity 89.8%; Pred. No. 1.2e-34;
Matches 97; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
||||||: ||| |||||||||| |||||||||||||||||||||||:|:| |||||||
Db 1 DIQMTQSPSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 60

Qy 61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
|||| |||||||||||||||||||||| |||: |||||||||||||
Db 61 RFSGSGSGTDYSLTISNLEPEDIATYFCQQYSEFPWTFGGGTKLEIKR 108

RESULT 12
AAW16620
ID AAW16620 standard; protein; 108 AA.
XX
AC AAW16620;
XX
DT 14-JAN-1998 (first entry)
XX
DE Anti-human FasL antibody (NOK1) light chain variable region.
XX
KW Light chain; variable region; mouse; murine; human; Fas ligand; FasL;
KW monoclonal antibody; MAb; hybridoma; treatment; hepatitis;
KW hepatitis B virus; HBV; hepatitis C virus; HCV; apoptosis; liver cell;
KW glutamate oxaloacetate; pyruvate transaminase.
XX
OS Mus sp.
XX
PN WO9715326-A1.
XX
PD 01-MAY-1997.
XX
PF 24-OCT-1996; 96WO-JP003089.
XX
PR 27-OCT-1995; 95JP-00303491.
XX
PA (SUME) SUMITOMO ELECTRIC IND CO.
XX
PI Seino K, Kayagaki N, Yagita H, Okumura K, Nakata M;
XX
DR WPI; 1997-258767/23.
DR N-PSDB; AAT66710.
XX
PT Anti-human Fas Ligand antibody to treat hepatitis - controls apoptosis in
PT liver cells and improves liver function.
XX
PS Claim 6; Page 30-31; 51pp; Japanese.
XX
CC The present sequence is the light chain variable region of the murine
CC anti-human Fas ligand (FasL) monoclonal antibody (MAb) NOK1, which is
CC expressed by the hybridoma NOK1 (FERM BP-5044). The MAb can be used in
CC the preparation of a composition for the effective oral or parenteral
CC treatment of hepatitis, including hepatitis caused by hepatitis B or C
CC virus. The composition controls apoptosis in liver cells caused by the
CC binding of FasL to Fas expressing liver cells, and improves liver
CC function by improving blood glutamate oxaloacetate and pyruvate
CC transaminase levels. The composition is given in a dosage of 0.0001-1000,
CC preferably 0.01-600 mg/day. Spleen cells from mice immunised with FasL
CC expressing COS cells were fused with mouse myeloma cells to produce
CC hybridomas. The hybridomas were screened for anti-FasL activity, and the
CC active clones NOK1-5 isolated
XX
SQ Sequence 108 AA;

Query Match 90.2%; Score 516; DB 2; Length 108;
Best Local Similarity 89.8%; Pred. No. 1.2e-34;
Matches 97; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
||||||: ||| |||||||||| |||||||||||||||||||||||:|:| |||||||
Db 1 DIQMTQSPSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 60

Qy 61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
|||| |||||||||||||||||||||| |||: |||||||||||||
Db 61 RFSGSGSGTDYSLTISNLEPEDIATYFCQQYSEFPWTFGGGTKLEIKR 108

RESULT 13
AAB81998
ID AAB81998 standard; protein; 128 AA.
XX
AC AAB81998;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein #7.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
DR N-PSDB; AAF86912.
XX

PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Example 3; Page 164-165; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 128 AA;

Query Match 90.2%; Score 516; DB 4; Length 128;
Best Local Similarity 88.9%; Pred. No. 1.4e-34;
Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
Db 21 DIQMTQSASSLPASVGDRVTITCSASQDISNYLNWYQQKPGKAVKLLIFYSSNLHSGVPS 80

Qy 61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
Db 81 RFSGGGSGTDYTLTISSLQPEDFATYFCHQYSKLPWTFGQGTKVEIKR 128

RESULT 14
ABR62591
ID ABR62591 standard; protein; 650 AA.
XX
AC ABR62591;
XX
DT 06-NOV-2003 (first entry)
XX
DE Anti-CD7 antibody TH-69 scFv-Pseudomonas exotoxin A fusion protein.
XX
KW CD7; antibody; TH-69; scFv; exotoxin A; immunotoxin; cytostatic;
KW immunosuppressive; vaccine.
XX
OS Mus sp.
OS Pseudomonas sp.
OS Synthetic.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Region 7. .265
FT /label= scFv
FT Region 125. .285
FT /label= Linker
FT Region 286. .646
FT /label= ETA
XX
PN WO2003051926-A2.
XX
PD 26-JUN-2003.
XX
PF 11-DEC-2002; 2002WO-EP014064.
XX
PR 14-DEC-2001; 2001US-0339422P.
XX
PA (UYER-) UNIV ERLANGEN-NUERNBERG.
XX
PI Fey GHM, Gramatzki M, Peipp M;
XX
DR WPI; 2003-523519/49.
DR N-PSDB; ACF05482.
XX
PT New fusion protein comprising functionally linked components of an anti-
PT CD7 antibody or its fragment and an immunotoxin, useful for treating CD7
PT positive acute T-cell and/or myeloid leukemias, or Graft-versus-host
PT disease.
XX
PS Claim 9; Page 8; 55pp; English.
XX
CC The present sequence is that of a novel fusion protein comprising an scFv
CC fragment of anti-CD7 monoclonal antibody TH-69 and domains II and III of
CC Pseudomonas exotoxin A (ETA), joined via a peptide linker, and including
CC an N-terminal 6xHis tag and C-terminal KDEL sequence. This novel fusion
CC protein binds to CD7-positive T-lymphoid cells and kills them by the
CC induction of apoptosis. It is an example of anti-CD7 scFv immunotoxin
CC fusion proteins of the invention. An expression vector, host cells, a
CC method for producing the fusion protein, and a vaccine comprising the
CC fusion protein are claimed. The fusion protein is used in the treatment
CC of disorders involved a hyperproliferation of CD7-positive cells,
CC especially acute T-cell and/or myeloid leukaemia, and also in the
CC treatment or prophylaxis of Graft-versus-host disease. A claimed method
CC of conditioning an animal (e.g. a human) to be transplanted with donor
CC cells, tissue or organ comprises: (a) depleting the CD7-bearing cell
CC population in the animal; (b) providing a transplant comprising isolated
CC bone marrow and/or stem cell-enriched peripheral blood cells of the
CC donor, where the CD7-bearing cell population in (a) and/or the transplant
CC in (b) are treated with a T-cell depleting effective amount of the fusion
CC protein or therapeutic composition comprising the fusion protein; and (c)
CC introducing the transplant into the animal
XX
SQ Sequence 650 AA;

Query Match 90.2%; Score 516; DB 6; Length 650;
Best Local Similarity 90.7%; Pred. No. 7.1e-34;
Matches 98; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
Db 17 DIQMTQTTSSLSASLGDRVTISCSASQGISNYLNWYQQKPDGTVKLLIYYTSSLHSGVPS 76

Qy 61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
Db 77 RFSGSGSGTDYSLTISNLEPEDIATYYCQQYSKLPYTFGGGTKLEIKR 124

RESULT 15
ABR62590
ID ABR62590 standard; protein; 651 AA.
XX
AC ABR62590;
XX
DT 06-NOV-2003 (first entry)
XX
DE Anti-CD7 antibody TH-69 scFv-Pseudomonas exotoxin A fusion protein.
XX
KW CD7; antibody; TH-69; scFv; exotoxin A; immunotoxin; cytostatic;
KW immunosuppressive; vaccine.
XX
OS Mus sp.
OS Pseudomonas sp.
OS Synthetic.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Region 7. .265
FT /label= scFv
FT Region 125. .285
FT /label= Linker
FT Region 286. .646
FT /label= ETA
XX
PN WO2003051926-A2.
XX
PD 26-JUN-2003.
XX
PF 11-DEC-2002; 2002WO-EP014064.
XX
PR 14-DEC-2001; 2001US-0339422P.
XX

PA (UYER-) UNIV ERLANGEN-NUERNBERG.
XX
PI Fey GHM, Gramatzki M, Peipp M;
XX
DR WPI; 2003-523519/49.
DR N-PSDB; ACF05481.
XX
PT New fusion protein comprising functionally linked components of an anti-
PT CD7 antibody or its fragment and an immunotoxin, useful for treating CD7
PT positive acute T-cell and/or myeloid leukemias, or Graft-versus-host
PT disease.
XX
PS Claim 9; Page 7; 55pp; English.
XX
CC The present sequence is that of a novel fusion protein comprising an scFv
CC fragment of anti-CD7 monoclonal antibody TH-69 and domains II and III of
CC Pseudomonas exotoxin A (ETA), joined via a peptide linker, and including
CC an N-terminal 6xHis tag and C-terminal REDLK sequence. This novel fusion
CC protein binds to CD7-positive T-lymphoid cells and kills them by the
CC induction of apoptosis. It is an example of anti-CD7 scFv immunotoxin
CC fusion proteins of the invention. An expression vector, host cells, a
CC method for producing the fusion protein, and a vaccine comprising the
CC fusion protein are claimed. The fusion protein is used in the treatment
CC of disorders involved a hyperproliferation of CD7-positive cells,
CC especially acute T-cell and/or myeloid leukaemia, and also in the
CC treatment or prophylaxis of Graft-versus-host disease. A claimed method
CC of conditioning an animal (e.g. a human) to be transplanted with donor
CC cells, tissue or organ comprises: (a) depleting the CD7-bearing cell
CC population in the animal; (b) providing a transplant comprising isolated
CC bone marrow and/or stem cell-enriched peripheral blood cells of the
CC donor, where the CD7-bearing cell population in (a) and/or the transplant
CC in (b) are treated with a T-cell depleting effective amount of the fusion
CC protein or therapeutic composition comprising the fusion protein; and (c)
CC introducing the transplant into the animal
XX
SQ Sequence 651 AA;

Query Match 90.2%; Score 516; DB 6; Length 651;
Best Local Similarity 90.7%; Pred. No. 7.1e-34;
Matches 98; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

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              ||||||| ||| ||||||||||||||| ||||||||||||||||||:|:|:|||||||
Db         17 DIQMTQTTSSLSASLGDRVTISCSASQGISNYLNWYQQKPDGTVKLLIYYTSSLHSGVPS 76

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              |||| |||||||||||||||||||:| ||||||:||||||||||||
Db         77 RFSGSGSGTDYSLTISNLEPEDIATYYCQQYSKLPYTFGGGTKLEIKR 124
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Job time : 30.8913 secs

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OM protein - protein search, using sw model

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(without alignments)
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Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	572	100.0	128	4	US-09-225-322B-10	Sequence 10, Appl
2	572	100.0	128	4	US-09-225-322B-19	Sequence 19, Appl
3	572	100.0	128	4	US-09-764-304-10	Sequence 10, Appl
4	572	100.0	128	4	US-09-764-304-19	Sequence 19, Appl
5	516	90.2	108	3	US-09-065-059-3	Sequence 3, Appli
6	503	87.9	107	2	US-08-652-558-35	Sequence 35, Appl
7	502	87.8	131	1	US-08-236-520-2	Sequence 2, Appli
8	502	87.8	131	5	PCT-US95-05262-2	Sequence 2, Appli
9	498	87.1	112	3	US-08-487-761-13	Sequence 13, Appl
10	497	86.9	109	4	US-09-386-658A-4	Sequence 4, Appli
11	488	85.3	107	1	US-08-458-516-9	Sequence 9, Appli
12	488	85.3	127	1	US-08-458-516-5	Sequence 5, Appli
13	488	85.3	127	3	US-08-649-100-17	Sequence 17, Appl
14	487	85.1	108	3	US-09-199-149-7	Sequence 7, Appli
15	487	85.1	274	4	US-09-813-659-30	Sequence 30, Appl
16	487	85.1	274	4	US-09-549-067A-30	Sequence 30, Appl
17	487	85.1	302	1	US-08-121-054C-18	Sequence 18, Appl
18	487	85.1	302	1	US-08-121-054C-30	Sequence 30, Appl
19	487	85.1	302	3	US-08-539-436-18	Sequence 18, Appl
20	487	85.1	302	3	US-08-539-436-30	Sequence 30, Appl
21	487	85.1	302	4	US-09-813-659-18	Sequence 18, Appl
22	487	85.1	302	4	US-09-813-659-32	Sequence 32, Appl
23	487	85.1	302	4	US-09-549-067A-18	Sequence 18, Appl
24	487	85.1	302	4	US-09-549-067A-32	Sequence 32, Appl
25	484	84.6	109	1	US-07-942-245-10	Sequence 10, Appl
26	483	84.4	107	2	US-07-934-373C-16	Sequence 16, Appl
27	483	84.4	107	3	US-08-437-642B-16	Sequence 16, Appl
28	483	84.4	107	4	US-08-146-206C-16	Sequence 16, Appl
29	483	84.4	107	4	US-09-705-686-16	Sequence 16, Appl
30	483	84.4	107	4	US-09-705-392A-16	Sequence 16, Appl
31	483	84.4	107	5	PCT-US93-07832-16	Sequence 16, Appl
32	483	84.4	127	1	US-08-137-117D-37	Sequence 37, Appl
33	483	84.4	127	2	US-08-436-717-37	Sequence 37, Appl
34	474	82.9	127	1	US-08-137-117D-29	Sequence 29, Appl
35	474	82.9	127	2	US-08-436-717-29	Sequence 29, Appl
36	469	82.0	214	1	US-08-425-763-1	Sequence 1, Appli
37	469	82.0	214	2	US-07-934-373C-24	Sequence 24, Appl
38	469	82.0	214	3	US-08-437-642B-24	Sequence 24, Appl
39	469	82.0	214	3	US-08-811-757-1	Sequence 1, Appli
40	469	82.0	214	3	US-09-249-230-1	Sequence 1, Appli
41	469	82.0	214	4	US-08-146-206C-24	Sequence 24, Appl
42	469	82.0	214	4	US-09-705-686-24	Sequence 24, Appl
43	469	82.0	214	4	US-09-705-392A-24	Sequence 24, Appl
44	469	82.0	214	5	PCT-US93-07832-24	Sequence 24, Appl
45	468	81.8	273	2	US-08-403-853-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-09-225-322B-10
; Sequence 10, Application US/09225322B
; Patent No. 6437098
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/225,322B
; CURRENT FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-09-225-322B-10

Query Match 100.0%; Score 572; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 3.5e-51;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 80

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 128
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RESULT 2
US-09-225-322B-19
; Sequence 19, Application US/09225322B

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; Patent No. 6437098
; GENERAL INFORMATION:
;  APPLICANT: SHITARA, KENYA
;  APPLICANT:  HANAI, NOBUO
;  APPLICANT:  HASEGAWA, MAMORU
;  APPLICANT:  MIYAJI, HIROMASA
;  APPLICANT:  KUWANA, YOSHIHISA
;  TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
;  FILE REFERENCE: 249-101
;  CURRENT APPLICATION NUMBER: US/09/225,322B
;  CURRENT FILING DATE:  1999-01-05
;  PRIOR APPLICATION NUMBER: US 08/454,680
;  PRIOR FILING DATE: 1995-05-31
;  PRIOR APPLICATION NUMBER: US 08/408,133
;  PRIOR FILING DATE: 1995-03-21
;  PRIOR APPLICATION NUMBER: US 08/292,178
;  PRIOR FILING DATE: 1994-08-17
;  PRIOR APPLICATION NUMBER: US07/947,674
;  PRIOR FILING DATE: 1992-09-17
;  PRIOR APPLICATION NUMBER: JP 3-238375
;  PRIOR FILING DATE: 1991-09-18
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
;   LENGTH: 128
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:light chain
;   OTHER INFORMATION: variable region
US-09-225-322B-19

  Query Match            100.0%;  Score 572;  DB 4;  Length 128;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-51;
  Matches  108;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
pb         21 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 80

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 128


RESULT 3
US-09-764-304-10
; Sequence 10, Application US/09764304
; Patent No. 6495666
; GENERAL INFORMATION:
;  APPLICANT: SHITARA, KENYA
;  APPLICANT: HANAI, NOBUO
;  APPLICANT: HASEGAWA, MAMORU
;  APPLICANT: MIYAJI, HIROMASA
;  APPLICANT: KUWANA, YOSHIHISA
;  TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
;  FILE REFERENCE: 249-101
;  CURRENT APPLICATION NUMBER: US/09/764,304
;  CURRENT FILING DATE: 2001-01-19
;  EARLIER APPLICATION NUMBER: 09/225,322
;  EARLIER FILING DATE: 1999-01-05
;  EARLIER APPLICATION NUMBER: US 08/454,680
;  EARLIER FILING DATE: 1995-05-31
;  EARLIER APPLICATION NUMBER: US 08/408,133
;  EARLIER FILING DATE: 1995-03-21
;  EARLIER APPLICATION NUMBER: US 08/292,178
;  EARLIER FILING DATE: 1994-08-17
;  EARLIER APPLICATION NUMBER: US07/947,674
;  EARLIER FILING DATE: 1992-09-17
;  EARLIER APPLICATION NUMBER: JP 3-238375
;  EARLIER FILING DATE: 1991-09-18
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 128
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: cDNA KM-641
US-09-764-304-10

  Query Match            100.0%;  Score 572;  DB 4;  Length 128;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-51;
  Matches  108;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 80

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 128


RESULT 4
US-09-764-304-19
; Sequence 19, Application US/09764304
; Patent No. 6495666
; GENERAL INFORMATION:
;  APPLICANT: SHITARA, KENYA
;  APPLICANT: HANAI, NOBUO
;  APPLICANT: HASEGAWA, MAMORU
;  APPLICANT: MIYAJI, HIROMASA
;  APPLICANT: KUWANA, YOSHIHISA
;  TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
;  FILE REFERENCE: 249-101
;  CURRENT APPLICATION NUMBER: US/09/764,304
;  CURRENT FILING DATE: 2001-01-19
;  EARLIER APPLICATION NUMBER: 09/225,322
;  EARLIER FILING DATE: 1999-01-05
;  EARLIER APPLICATION NUMBER: US 08/454,680
;  EARLIER FILING DATE: 1995-05-31
;  EARLIER APPLICATION NUMBER: US 08/408,133
;  EARLIER FILING DATE: 1995-03-21
;  EARLIER APPLICATION NUMBER: US 08/292,178
;  EARLIER FILING DATE: 1994-08-17
;  EARLIER APPLICATION NUMBER: US07/947,674
;  EARLIER FILING DATE: 1992-09-17
;  EARLIER APPLICATION NUMBER: JP 3-238375
;  EARLIER FILING DATE: 1991-09-18
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
;   LENGTH: 128
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: light chain
;   OTHER INFORMATION: variable region
US-09-764-304-19

  Query Match            100.0%;  Score 572;  DB 4;  Length 128;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-51;
  Matches  108;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 80

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 128


RESULT 5
US-09-065-059-3
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; Sequence 3, Application US/09065059
; Patent No. 6068841
; GENERAL INFORMATION:
;   APPLICANT:  SEINO, Ken-ichiro
;   APPLICANT:  KAYAGAKI, No. 6068841uhiko
;   APPLICANT:  YAGITA, Hideo
;   APPLICANT:  OKUMURA, Ko
;   APPLICANT:  NAKATA, Motomi
;   TITLE OF INVENTION:  THERAPEUTIC AGENT FOR HEPATITIS
;   NUMBER OF SEQUENCES:  18
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  McDermott, Will & Emery
;     STREET:  99 Canal Center Plaza
;     CITY:  Alexandria
;     STATE:  Virginia
;     COUNTRY:  USA
;     ZIP:  22314
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/09/065,059
;     FILING DATE:
;     CLASSIFICATION:  424
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Bucca Ph.D., Daniel
;     REGISTRATION NUMBER:  P-42,368
;     REFERENCE/DOCKET NUMBER:  50356-151
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  703-518-5100
;     TELEFAX:  703-684-1124
; INFORMATION FOR SEQ ID NO:  3:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  108 amino acids
;     TYPE:  amino acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
US-09-065-059-3

  Query Match             90.2%;  Score 516;  DB 3;  Length 108;
  Best Local Similarity   89.8%;  Pred. No. 1.5e-45;
  Matches   97;  Conservative    4;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||: ||| |||||||||| |||||||||||||||||||||:|:| |||||||
Db          1 DIQMTQSPSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 60

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              |||| |||||||||||||||||||||| |||: |||||||||||||||
Db         61 RFSGSGSGTDYSLTISNLEPEDIATYFCQQYSEFPWTFGGGTKLEIKR 108


RESULT 6
US-08-652-558-35
; Sequence 35, Application US/08652558
; Patent No. 5861155
; GENERAL INFORMATION:
;   APPLICANT:  LIN, AUGUSTINE YEE-THARN
;   TITLE OF INVENTION:  HUMANIZED ANTIBODIES AND USES
;   TITLE OF INVENTION:  THEREOF
;   NUMBER OF SEQUENCES:  52
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  BANNER & WITCOFF
;     STREET:  75 STATE STREET, 23RD FLOOR
;     CITY:  BOSTON
;     STATE:  MASSACHUSETTS
;     COUNTRY:  USA
;     ZIP:  02109
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  3.5 inch diskette, 1.4 Mb storage
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  WordPerfect 6.1
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/652,558
;     FILING DATE:  JUNE 6, 1996
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  PCT/IB94/00387
;     FILING DATE:  NOVEMBER 21, 1994
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  YANKWICH, LEON R.
;     REGISTRATION NUMBER:  30,237
;     REFERENCE/DOCKET NUMBER:  95,497-L
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  617-345-9100
;     TELEFAX:  617-345-9111
; INFORMATION FOR SEQ ID NO:  35:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  107 amino acids
;     TYPE:  amino acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
US-08-652-558-35

  Query Match             87.9%;  Score 503;  DB 2;  Length 107;
  Best Local Similarity   89.7%;  Pred. No. 3.2e-44;
  Matches   96;  Conservative    5;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||| ||| |||||||||||||| |||||||||||||||||||:|:|:|||||||
Db          1 DIQMTQTTSSLSASLGDRVTISCSASQGISNYLNWYQQKPDGTVKLLIYYTSSLHSGVPS 60

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIK 107
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Db         61 RFSGSGSGTDYSLTISNLEPEDIATYYCQQYSKLPRTFGGGTKVEIK 107


RESULT 7
US-08-236-520-2
; Sequence 2, Application US/08236520
; Patent No. 5591629
; GENERAL INFORMATION:
;   APPLICANT:  Rodriguez, Moses
;   APPLICANT:  Miller, David J.
;   TITLE OF INVENTION:  MONOCLONAL ANTIBODIES WHICH PROMOTE
;   TITLE OF INVENTION:  CENTRAL NERVOUS SYSTEM REMYELINATION
;   NUMBER OF SEQUENCES:  11
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Hamilton, Brook, Smithy & Reynolds, P.C.
;     STREET:  Two Militia Drive
;     CITY:  Lexington
;     STATE:  Massachusetts
;     COUNTRY:  USA
;     ZIP:  02173
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/236,520
;     FILING DATE:  29-APR-1994
;     CLASSIFICATION:  424
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Granahan, Patricia
;     REGISTRATION NUMBER:  27,227
;     REFERENCE/DOCKET NUMBER:  MMV92-01
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  617-861-6240
;     TELEFAX:  617-861-9540
; INFORMATION FOR SEQ ID NO:  2:
;   SEQUENCE CHARACTERISTICS:
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;      LENGTH:  131 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-236-520-2

  Query Match             87.8%;  Score 502;  DB 1;  Length 131;
  Best Local Similarity   88.9%;  Pred. No. 5.2e-44;
  Matches   96;  Conservative    3;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||| ||| |||||||||||| |||||||||||||||||||||||:|:| |||||||
Db         21 DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 80

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              |||| |||||||||||||| |||||||| | : |||||||||||||||
Db         81 RFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPWTFGGGTKLEIKR 128


RESULT 8
PCT-US95-05262-2
; Sequence 2, Application PC/TUS9505262
;  GENERAL INFORMATION:
;    APPLICANT:  Mayo Foundation for Medical Education Research
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES WHICH PROMOTE
;    TITLE OF INVENTION:  CENTRAL NERVOUS SYSTEM REMYELINATION
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smithy & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/05262
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  U.S. 08/236,520
;      FILING DATE:  April 29, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Granahan, Patricia
;      REGISTRATION NUMBER:  27,227
;      REFERENCE/DOCKET NUMBER:  MMV92-01 PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-861-6240
;      TELEFAX:  617-861-9540
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  131 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-05262-2

  Query Match             87.8%;  Score 502;  DB 5;  Length 131;
  Best Local Similarity   88.9%;  Pred. No. 5.2e-44;
  Matches   96;  Conservative    3;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||| ||| |||||||||||| |||||||||||||||||||||||:|:| |||||||
Db         21 DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 80

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              |||| |||||||||||||| |||||||| | : |||||||||||||||
Db         81 RFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPWTFGGGTKLEIKR 128


RESULT 9
US-08-487-761-13
; Sequence 13, Application US/08487761
; Patent No. 6217866
;  GENERAL INFORMATION:
;    APPLICANT:  Schlessinger, Joseph
;    APPLICANT:  Givol, David
;    APPLICANT:  Bellot, Francoise
;    APPLICANT:  Kris, Richard
;    APPLICANT:  Ricca, George A.
;    APPLICANT:  Cheadle, Christopher
;    APPLICANT:  South, Victoria J.
;    TITLE OF INVENTION:  Monoclonal Antibodies Specific to Human
;    TITLE OF INVENTION:  Epidermal Growth Factor Receptor and Therapeutic Methods
;    TITLE OF INVENTION:  Employing Same
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Rhone-Poulenc Rorer Inc.
;      STREET:  500 Arcola Road, 3C43
;      CITY:  Collegeville
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19426
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Macintosh
;      OPERATING SYSTEM:  System 7.1
;      SOFTWARE:  Word 5.0 (PatentIn)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/487,761
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/086,411
;      FILING DATE:  29-JUN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Goodman, Rosanne
;      REGISTRATION NUMBER:  32,534
;      REFERENCE/DOCKET NUMBER:  A0207C-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 454-3817
;      TELEFAX:  (215) 454-3808
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  112 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-487-761-13

  Query Match             87.1%;  Score 498;  DB 3;  Length 112;
  Best Local Similarity   87.0%;  Pred. No. 1.1e-43;
  Matches   94;  Conservative    6;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              :| |||| ||| |||||||||||||||| |||||||||||||||||:|:| |||||||
Db          1 EIHMTQTTSSLSASLGDRVTISCSASQDIRNYLNWYQQKPDGTVKLLIYYTSTLHSGVPS 60

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              |||| |||||||||||||||||||:| |||||:|:|| |||||||||
Db         61 RFSGSGSGTDYSLTISNLEPEDIATYYCQQYSKIPYTFTGGTKLEIKR 108


RESULT 10
US-09-386-658A-4
; Sequence 4, Application US/09386658A
; Patent No. 6593137
; GENERAL INFORMATION:
;  APPLICANT: Erlanger, Bernard F.
;  APPLICANT:  Chen, Bi-Xing
;  TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR FULLERENES
;  FILE REFERENCE: 0575/54182
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;  CURRENT APPLICATION NUMBER: US/09/386,658A
;  CURRENT FILING DATE:  1999-08-31
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 109
;   TYPE: PRT
;   ORGANISM: Mouse
US-09-386-658A-4

  Query Match            86.9%;  Score 497;  DB 4;  Length 109;
  Best Local Similarity  86.1%;  Pred. No. 1.3e-43;
  Matches   93;  Conservative    8;  Mismatches    7;  Indels    0;  Gaps    0;

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Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
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Db         61 RFSGSGSGTDYSLTINNLEPEDIATYFCQQYSRLPFTFGSGTKLEIKR 108


RESULT 11
US-08-458-516-9
; Sequence 9, Application US/08458516
; Patent No. 5777085
;  GENERAL INFORMATION:
;    APPLICANT:  Co, Man Sung
;    APPLICANT:  Tso, J. Yun
;    TITLE OF INVENTION:  Humanized Antibodies Reactive with
;    TITLE OF INVENTION:  GPIIB/IIIA
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  William M. Smith
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/458,516
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/059,159
;      FILING DATE:  03-MAY-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11823-37-3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-326-2400
;      TELEFAX:  415-326-2422
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-458-516-9

  Query Match            85.3%;  Score 488;  DB 1;  Length 107;
  Best Local Similarity  86.9%;  Pred. No. 1.1e-42;
  Matches   93;  Conservative    4;  Mismatches   10;  Indels    0;  Gaps    0;

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Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIK 107
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RESULT 12
US-08-458-516-5
; Sequence 5, Application US/08458516
; Patent No. 5777085
;  GENERAL INFORMATION:
;    APPLICANT:  Co, Man Sung
;    APPLICANT:  Tso, J. Yun
;    TITLE OF INVENTION:  Humanized Antibodies Reactive with
;    TITLE OF INVENTION:  GPIIB/IIIA
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  William M. Smith
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/458,516
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/059,159
;      FILING DATE:  03-MAY-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11823-37-3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-326-2400
;      TELEFAX:  415-326-2422
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  127 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-458-516-5

  Query Match            85.3%;  Score 488;  DB 1;  Length 127;
  Best Local Similarity  86.9%;  Pred. No. 1.3e-42;
  Matches   93;  Conservative    4;  Mismatches   10;  Indels    0;  Gaps    0;

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Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIK 107
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RESULT 13
US-08-649-100-17
; Sequence 17, Application US/08649100
; Patent No. 6114507
;  GENERAL INFORMATION:
;    APPLICANT:  SHIRAKAWA, KAMON
;    APPLICANT:  MATUSUE, TOMOKAZU
;    APPLICANT:  NAGATA, SHIGEKAZU
;    APPLICANT:  CO, MAN SUNG
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;    APPLICANT:  VASQUEZ, MAXIMILIANO
;    TITLE OF INVENTION:  ANTI-FAS LIGAND ANTIBODY AND ASSAY
;    TITLE OF INVENTION:  METHOD USING THE ANTI-FAS LIGAND ANTIBODY
;    NUMBER OF SEQUENCES:  41
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BIRCH, STEWART, KOLASCH AND BIRCH
;      STREET:  PO BOX 747
;      CITY:  FALLS CHURCH
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22040-0747
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/649,100
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURPHY JR, GERALD M
;      REGISTRATION NUMBER:  28,977
;      REFERENCE/DOCKET NUMBER:  1110-160
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 205-8000
;      TELEFAX:  (703) 205-8050
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  127 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-649-100-17

  Query Match             85.3%;  Score 488;  DB 3;  Length 127;
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Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIK 107
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Db         81 RFSGSGSGTNYSLTISNLEQGDIATYFCQQGSTLPWTFGGGTKLEIK 127


RESULT 14
US-09-199-149-7
; Sequence 7, Application US/09199149
; Patent No. 6160099
; GENERAL INFORMATION:
;  APPLICANT: Jonak, Zdenka L.
;  APPLICANT: Taylor, Alexander H.
;  APPLICANT: Trulli Jr., Stephen H.
;  APPLICANT: Johanson, Kyung O.
;  TITLE OF INVENTION: Humanized Monoclonal Antibodies
;  FILE REFERENCE: P50860
;  CURRENT APPLICATION NUMBER: US/09/199,149
;  CURRENT FILING DATE: 1998-11-24
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 108
;   TYPE: PRT
;   ORGANISM: murine cells
US-09-199-149-7

  Query Match             85.1%;  Score 487;  DB 3;  Length 108;
  Best Local Similarity   85.2%;  Pred. No. 1.4e-42;
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Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
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RESULT 15
US-09-813-659-30
; Sequence 30, Application US/09813659
; Patent No. 6482919
; GENERAL INFORMATION:
;  APPLICANT: Ledbetter, Jeffrey A.
;  APPLICANT:  Hayden, Martha S.
;  APPLICANT:  Linsley, Peter S.
;  APPLICANT:  Bajorath, Jurgen
;  APPLICANT:  Fell, H. Perry
;  APPLICANT:  Gilliland, Lisa K.
;  TITLE OF INVENTION: EXPRESSION VECTORS ENCODING BISPECIFIC FUSION PROTEINS
;  TITLE OF INVENTION:  AND METHODS OF PRODUCING BIOLOGICALLY ACTIVE BISPECIFIC
;  TITLE OF INVENTION:  FUSION PROTEINS IN A MAMMALIAN CELL
;  FILE REFERENCE: 30436.18USD2
;  CURRENT APPLICATION NUMBER: US/09/813,659
;  CURRENT FILING DATE:  2001-03-21
;  PRIOR APPLICATION NUMBER: 09/549,067
;  PRIOR FILING DATE: 2000-04-13
;  PRIOR APPLICATION NUMBER: 08/539,436
;  PRIOR FILING DATE: 1995-10-05
;  PRIOR APPLICATION NUMBER: 08/121,054
;  PRIOR FILING DATE: 1993-09-13
;  PRIOR APPLICATION NUMBER: 08/013,420
;  PRIOR FILING DATE: 1993-02-01
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
;   LENGTH: 274
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-813-659-30

  Query Match             85.1%;  Score 487;  DB 4;  Length 274;
  Best Local Similarity   85.2%;  Pred. No. 4.3e-42;
  Matches   92;  Conservative    5;  Mismatches   11;  Indels    0;  Gaps    0;

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

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Title: US-10-089-500-56
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	572	100.0	128	9	US-09-764-304-19	Sequence 19, Appl
3	572	100.0	128	14	US-10-265-713-10	Sequence 10, Appl
4	572	100.0	128	14	US-10-265-713-19	Sequence 19, Appl
5	572	100.0	128	14	US-10-166-626-10	Sequence 10, Appl
6	572	100.0	128	14	US-10-166-626-19	Sequence 19, Appl
7	510	89.2	108	9	US-09-056-160B-10	Sequence 10, Appl
8	510	89.2	108	14	US-10-234-671-10	Sequence 10, Appl
9	502	87.8	131	8	US-08-779-784-21	Sequence 21, Appl
10	502	87.8	131	14	US-10-010-729-64	Sequence 64, Appl
11	497	86.9	109	14	US-10-197-080-4	Sequence 4, Appli
12	494	86.4	107	17	US-10-741-657A-16	Sequence 16, Appl
13	491	85.8	107	17	US-10-473-977-69	Sequence 69, Appl
14	488	85.3	107	15	US-10-411-037-52	Sequence 52, Appl
15	488	85.3	107	15	US-10-411-026-52	Sequence 52, Appl
16	488	85.3	107	15	US-10-410-962-52	Sequence 52, Appl
17	488	85.3	107	15	US-10-411-049-52	Sequence 52, Appl
18	488	85.3	107	16	US-10-410-930-52	Sequence 52, Appl
19	488	85.3	107	16	US-10-410-997-52	Sequence 52, Appl
20	488	85.3	107	16	US-10-411-012-52	Sequence 52, Appl
21	488	85.3	107	16	US-10-287-994-52	Sequence 52, Appl
22	488	85.3	107	16	US-10-410-913-52	Sequence 52, Appl
23	488	85.3	108	13	US-10-140-555-4	Sequence 4, Appli
24	488	85.3	127	14	US-10-084-139-2	Sequence 2, Appli
25	488	85.3	601	9	US-09-480-236-1	Sequence 1, Appli
26	488	85.3	637	16	US-10-296-085A-16	Sequence 16, Appl
27	488	85.3	638	16	US-10-296-085A-21	Sequence 21, Appl
28	488	85.3	642	16	US-10-296-085A-38	Sequence 38, Appl
29	488	85.3	643	16	US-10-296-085A-69	Sequence 69, Appl
30	488	85.3	656	16	US-10-296-085A-39	Sequence 39, Appl
31	488	85.3	657	16	US-10-296-085A-68	Sequence 68, Appl
32	487	85.1	108	14	US-10-141-908-7	Sequence 7, Appli
33	487	85.1	274	9	US-09-813-659-30	Sequence 30, Appl
34	487	85.1	274	14	US-10-283-610A-30	Sequence 30, Appl
35	487	85.1	302	9	US-09-813-659-18	Sequence 18, Appl
36	487	85.1	302	9	US-09-813-659-32	Sequence 32, Appl
37	487	85.1	302	14	US-10-283-610A-18	Sequence 18, Appl
38	487	85.1	302	14	US-10-283-610A-32	Sequence 32, Appl
39	487	85.1	504	14	US-10-207-655-348	Sequence 348, App
40	487	85.1	555	15	US-10-107-991B-3	Sequence 3, Appli
41	485	84.8	107	14	US-10-310-674A-34	Sequence 34, Appl
42	485	84.8	107	15	US-10-389-679-10	Sequence 10, Appl
43	484	84.6	107	14	US-10-269-010-2	Sequence 2, Appli
44	484	84.6	107	14	US-10-268-883-6	Sequence 6, Appli
45	484	84.6	127	14	US-10-268-883-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-764-304-10
; Sequence 10, Application US/09764304
; Patent No. US20020026036A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUWANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; CURRENT FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cDNA KM-641
US-09-764-304-10

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  Best Local Similarity  100.0%;  Pred. No. 3.5e-45;
  Matches  108;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
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RESULT 2
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; Sequence 19, Application US/09764304
; Patent No. US20020026036A1
; GENERAL INFORMATION:
;  APPLICANT: SHITARA, KENYA
;  APPLICANT: HANAI, NOBUO
;  APPLICANT: HASEGAWA, MAMORU
;  APPLICANT: MIYAJI, HIROMASA
;  APPLICANT: KUWANA, YOSHIHISA
;  TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
;  FILE REFERENCE: 249-101
;  CURRENT APPLICATION NUMBER: US/09/764,304
;  CURRENT FILING DATE: 2001-01-19
;  EARLIER APPLICATION NUMBER: 09/225,322
;  EARLIER FILING DATE: 1999-01-05
;  EARLIER APPLICATION NUMBER: US 08/454,680
;  EARLIER FILING DATE: 1995-05-31
;  EARLIER APPLICATION NUMBER: US 08/408,133
;  EARLIER FILING DATE: 1995-03-21
;  EARLIER APPLICATION NUMBER: US 08/292,178
;  EARLIER FILING DATE: 1994-08-17
;  EARLIER APPLICATION NUMBER: US07/947,674
;  EARLIER FILING DATE: 1992-09-17
;  EARLIER APPLICATION NUMBER: JP 3-238375
;  EARLIER FILING DATE: 1991-09-18
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
;   LENGTH: 128
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: light chain
;   OTHER INFORMATION: variable region
US-09-764-304-19

  Query Match           100.0%;  Score 572;  DB 9;  Length 128;
  Best Local Similarity  100.0%;  Pred. No. 3.5e-45;
  Matches  108;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 80

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 128


RESULT 3
US-10-265-713-10
; Sequence 10, Application US/10265713
; Publication No. US20030095964A1
; GENERAL INFORMATION:
;  APPLICANT: SHITARA, KENYA
;  APPLICANT:  HANAI, NOBUO
;  APPLICANT:  HASEGAWA, MAMORU
;  APPLICANT:  MIYAJI, HIROMASA
;  APPLICANT:  KUWANA, YOSHIHISA
;  TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
;  FILE REFERENCE: 249-101
;  CURRENT APPLICATION NUMBER: US/10/265,713
;  CURRENT FILING DATE:  2002-10-08
;  PRIOR APPLICATION NUMBER: US/09/225,322
;  PRIOR FILING DATE: 1999-01-05
;  PRIOR APPLICATION NUMBER: US 08/454,680
;  PRIOR FILING DATE: 1995-05-31
;  PRIOR APPLICATION NUMBER: US 08/408,133
;  PRIOR FILING DATE: 1995-03-21
;  PRIOR APPLICATION NUMBER: US 08/292,178
;  PRIOR FILING DATE: 1994-08-17
;  PRIOR APPLICATION NUMBER: US07/947,674
;  PRIOR FILING DATE: 1992-09-17
;  PRIOR APPLICATION NUMBER: JP 3-238375
;  PRIOR FILING DATE: 1991-09-18
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 128
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-10-265-713-10

  Query Match           100.0%;  Score 572;  DB 14;  Length 128;
  Best Local Similarity  100.0%;  Pred. No. 3.5e-45;
  Matches  108;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 80

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 128


RESULT 4
US-10-265-713-19
; Sequence 19, Application US/10265713
; Publication No. US20030095964A1
; GENERAL INFORMATION:
;  APPLICANT: SHITARA, KENYA
;  APPLICANT:  HANAI, NOBUO
;  APPLICANT:  HASEGAWA, MAMORU
;  APPLICANT:  MIYAJI, HIROMASA
;  APPLICANT:  KUWANA, YOSHIHISA
;  TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
;  FILE REFERENCE: 249-101
;  CURRENT APPLICATION NUMBER: US/10/265,713
;  CURRENT FILING DATE:  2002-10-08
;  PRIOR APPLICATION NUMBER: US/09/225,322
;  PRIOR FILING DATE: 1999-01-05
;  PRIOR APPLICATION NUMBER: US 08/454,680
;  PRIOR FILING DATE: 1995-05-31
;  PRIOR APPLICATION NUMBER: US 08/408,133
;  PRIOR FILING DATE: 1995-03-21
;  PRIOR APPLICATION NUMBER: US 08/292,178
;  PRIOR FILING DATE: 1994-08-17
;  PRIOR APPLICATION NUMBER: US07/947,674
;  PRIOR FILING DATE: 1992-09-17
;  PRIOR APPLICATION NUMBER: JP 3-238375
;  PRIOR FILING DATE: 1991-09-18
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
;   LENGTH: 128
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:light chain
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;   OTHER INFORMATION: variable region
US-10-265-713-19

  Query Match             100.0%;  Score 572;  DB 14;  Length 128;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-45;
  Matches  108;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 80

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 128


RESULT 5
US-10-166-626-10
; Sequence 10, Application US/10166626
; Publication No. US20030166876A1
; GENERAL INFORMATION:
;  APPLICANT: SHITARA, KENYA
;  APPLICANT:  HANAI, NOBUO
;  APPLICANT:  HASEGAWA, MAMORU
;  APPLICANT:  MIYAJI, HIROMASA
;  APPLICANT:  KUWANA, YOSHIHISA
;  TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
;  FILE REFERENCE: 249-101
;  CURRENT APPLICATION NUMBER: US/10/166,626
;  CURRENT FILING DATE:  2002-06-12
;  PRIOR APPLICATION NUMBER: US/09/225,322B
;  PRIOR FILING DATE: 1999-01-05
;  PRIOR APPLICATION NUMBER: US 08/454,680
;  PRIOR FILING DATE: 1995-05-31
;  PRIOR APPLICATION NUMBER: US 08/408,133
;  PRIOR FILING DATE: 1995-03-21
;  PRIOR APPLICATION NUMBER: US 08/292,178
;  PRIOR FILING DATE: 1994-08-17
;  PRIOR APPLICATION NUMBER: US07/947,674
;  PRIOR FILING DATE: 1992-09-17
;  PRIOR APPLICATION NUMBER: JP 3-238375
;  PRIOR FILING DATE: 1991-09-18
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 128
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-10-166-626-10

  Query Match             100.0%;  Score 572;  DB 14;  Length 128;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-45;
  Matches  108;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 80

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 128


RESULT 6
US-10-166-626-19
; Sequence 19, Application US/10166626
; Publication No. US20030166876A1
; GENERAL INFORMATION:
;  APPLICANT: SHITARA, KENYA
;  APPLICANT:  HANAI, NOBUO
;  APPLICANT:  HASEGAWA, MAMORU
;  APPLICANT:  MIYAJI, HIROMASA
;  APPLICANT:  KUWANA, YOSHIHISA
;  TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
;  FILE REFERENCE: 249-101
;  CURRENT APPLICATION NUMBER: US/10/166,626
;  CURRENT FILING DATE:  2002-06-12
;  PRIOR APPLICATION NUMBER: US/09/225,322B
;  PRIOR FILING DATE: 1999-01-05
;  PRIOR APPLICATION NUMBER: US 08/454,680
;  PRIOR FILING DATE: 1995-05-31
;  PRIOR APPLICATION NUMBER: US 08/408,133
;  PRIOR FILING DATE: 1995-03-21
;  PRIOR APPLICATION NUMBER: US 08/292,178
;  PRIOR FILING DATE: 1994-08-17
;  PRIOR APPLICATION NUMBER: US07/947,674
;  PRIOR FILING DATE: 1992-09-17
;  PRIOR APPLICATION NUMBER: JP 3-238375
;  PRIOR FILING DATE: 1991-09-18
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
;   LENGTH: 128
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:light chain
;   OTHER INFORMATION: variable region
US-10-166-626-19

  Query Match             100.0%;  Score 572;  DB 14;  Length 128;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-45;
  Matches  108;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 80

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 128


RESULT 7
US-09-056-160B-10
; Sequence 10, Application US/09056160B
; Patent No. US20020032315A1
;  GENERAL INFORMATION:
;    APPLICANT:  Baca, Manuel
;    APPLICANT:  Wells, James A.
;    APPLICANT:  Presta, Leonard G.
;    APPLICANT:  Lowman, Henry B.
;    APPLICANT:  Chen, Yvonne M.
;    TITLE OF INVENTION:  ANTI-VEGF ANTIBODIES
;    NUMBER OF SEQUENCES:  131
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/056,160B
;      FILING DATE:  06-Apr-1998
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/054,856
;      FILING DATE:  06-AUG-1997
```

```
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  P1093R2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-1896
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  108 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-09-056-160B-10

  Query Match             89.2%;  Score 510;  DB 9;  Length 108;
  Best Local Similarity   88.0%;  Pred. No. 1.6e-39;
  Matches   95;  Conservative    7;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||| ||| ||||||| |||||||||||||||||||||||:||:::|:|||||||
Db          1 DIQMTQTTSSLSASLGDRVIISCSASQDISNYLNWYQQKPDGTVKVLIYFTSSLHSGVPS 60

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              |||| |||||||||||||||||||:| ||| :|||||||||||||||
Db         61 RFSGSGSGTDYSLTISNLEPEDIATYYCQQYSTVPWTFGGGTKLEIKR 108


RESULT 8
US-10-234-671-10
; Sequence 10, Application US/10234671
; Publication No. US20030190317A1
;   GENERAL INFORMATION:
;        APPLICANT: Baca, Manuel
;                   Wells, James A.
;                   Presta, Leonard G.
;                   Lowman, Henry B.
;                   Chen, Yvonne M.
;        TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
;        NUMBER OF SEQUENCES: 131
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Genentech, Inc.
;             STREET: 1 DNA Way
;             CITY: South San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94080
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: WinPatin (Genentech)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/234,671
;             FILING DATE: 03-Sep-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/056160
;             FILING DATE: 06-APR-1998
;             APPLICATION NUMBER: 60/126446
;             FILING DATE: 07-APR-1997
;             APPLICATION NUMBER: 60/054856
;             FILING DATE: 06-AUG-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Cui, Steven X.
;             REGISTRATION NUMBER: 44,637
;             REFERENCE/DOCKET NUMBER: P1093R2C1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650/225-8674
;             TELEFAX: 650/952-9881
;   INFORMATION FOR SEQ ID NO: 10:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 108 amino acids
;             TYPE: Amino Acid
;             TOPOLOGY: Linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-234-671-10

  Query Match             89.2%;  Score 510;  DB 14;  Length 108;
  Best Local Similarity   88.0%;  Pred. No. 1.6e-39;
  Matches   95;  Conservative    7;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||| ||| ||||||| |||||||||||||||||||||||:||:::|:|||||||
Db          1 DIQMTQTTSSLSASLGDRVIISCSASQDISNYLNWYQQKPDGTVKVLIYFTSSLHSGVPS 60

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              |||| |||||||||||||||||||:| ||| :|||||||||||||||
Db         61 RFSGSGSGTDYSLTISNLEPEDIATYYCQQYSTVPWTFGGGTKLEIKR 108


RESULT 9
US-08-779-784-21
; Sequence 21, Application US/08779784
; Publication No. US20020164325A1
;  GENERAL INFORMATION:
;    APPLICANT:  Rodriguez, Moses
;    APPLICANT:  Miller, David J.
;    APPLICANT:  Asakura, Kunihiko
;    TITLE OF INVENTION:  PROMOTION OF CENTRAL NERVOUS SYSTEM
;    TITLE OF INVENTION:  REMYELINATION USING MONOCLONAL AUTOANTIBODIES
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  David A. Jackson, Esq.
;      STREET:  411 Hackensack Ave, Continental Plaza, 4th
;      STREET:  Floor
;      CITY:  Hackensack
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/779,784
;      FILING DATE:  07-JAN-1997
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/692,084
;      FILING DATE:  08-AUG-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/236,520
;      FILING DATE:  29-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jackson Esq., David A.
;      REGISTRATION NUMBER:  26,742
;      REFERENCE/DOCKET NUMBER:  1199-1-001 CIPA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-487-5800
;      TELEFAX:  201-343-1684
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  131 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-779-784-21

  Query Match             87.8%;  Score 502;  DB 8;  Length 131;
  Best Local Similarity   88.9%;  Pred. No. 1e-38;
  Matches   96;  Conservative    3;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||| ||| |||||||||| |||||||||||||||||||||:|:| |||||||
Db         21 DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 80
```

```
Qy          61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
               |||| ||||||||||||||| |||||||| | : |||||||||||||||
Db          81 RFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPWTFGGGTKLEIKR 128


RESULT 10
US-10-010-729-64
; Sequence 64, Application US/10010729
; Publication No. US20030185827A1
; GENERAL INFORMATION:
;  APPLICANT: Rodriguez, Moses
;  APPLICANT:  Miller, David J.
;  APPLICANT:  Pease, Larry R.
;  TITLE OF INVENTION: Human IgM Antibodies and Diagnostic and
;  TITLE OF INVENTION:  Therapeutic Uses Thereof Particularly in the Central Nervous
;  TITLE OF INVENTION:  System
;  FILE REFERENCE: 1199-1-005CIP2
;  CURRENT APPLICATION NUMBER: US/10/010,729
;  CURRENT FILING DATE:  2001-11-13
;  PRIOR APPLICATION NUMBER: 09/730,473
;  PRIOR FILING DATE: 2000-12-05
;  PRIOR APPLICATION NUMBER: 09/580,787
;  PRIOR FILING DATE: 2000-05-30
;  PRIOR APPLICATION NUMBER: 09/322,862
;  PRIOR FILING DATE: 1999-05-28
;  PRIOR APPLICATION NUMBER: 08/779,784
;  PRIOR FILING DATE: 1997-01-07
;  PRIOR APPLICATION NUMBER: 08/692,084
;  PRIOR FILING DATE: 1996-08-08
;  PRIOR APPLICATION NUMBER: 08/236,520
;  PRIOR FILING DATE: 1994-04-29
;  NUMBER OF SEQ ID NOS: 80
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 64
;   LENGTH: 131
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-010-729-64

  Query Match             87.8%;  Score 502;  DB 14;  Length 131;
  Best Local Similarity   88.9%;  Pred. No. 1e-38;
  Matches   96;  Conservative    3;  Mismatches    9;  Indels    0;  Gaps    0;

Qy           1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
               ||||||| ||| |||||||||||| |||||||||||||||||||||||:|:| |||||||
Db          21 DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 80

Qy          61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
               |||| ||||||||||||| |||||||| | : |||||||||||||||
Db          81 RFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPWTFGGGTKLEIKR 128


RESULT 11
US-10-197-080-4
; Sequence 4, Application US/10197080
; Publication No. US20030113940A1
; GENERAL INFORMATION:
;  APPLICANT: Erlanger, Bernard F.
;  APPLICANT:  Sheetz, Michael
;  APPLICANT:  Brus, Louis
;  TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NANOTUBES AND RELATED METHODS AND COMPOSI
;  FILE REFERENCE: 0575/67096-A
;  CURRENT APPLICATION NUMBER: US/10/197,080
;  CURRENT FILING DATE:  2002-07-16
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 109
;   TYPE: PRT
;   ORGANISM: Mouse
US-10-197-080-4

  Query Match             86.9%;  Score 497;  DB 14;  Length 109;
  Best Local Similarity   86.1%;  Pred. No. 2.5e-38;
  Matches   93;  Conservative    8;  Mismatches    7;  Indels    0;  Gaps    0;

Qy           1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
               ||||||| ||| |||||||| ||||||||:|||||||||||||:||||:|:|:| |||||
Db           1 DIQMTQTTSSLSASLGDRVTFSCSASQDINNYLNWYQQKPDGTIKLLIYYTSSLRSGVPS 60

Qy          61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
               |||| ||||||||||:|||||||||||| |||:||:||| ||||||||
Db          61 RFSGSGSGTDYSLTINNLEPEDIATYFCQQYSRLPFTFGSGTKLEIKR 108


RESULT 12
US-10-741-657A-16
; Sequence 16, Application US/10741657A
; Publication No. US20040197325A1
; GENERAL INFORMATION:
;  APPLICANT: Protein Design Labs
;  TITLE OF INVENTION: ANTIBODIES AGAINST GPR64 AND USES THEREOF
;  FILE REFERENCE: 05882.0177.NPUS01
;  CURRENT APPLICATION NUMBER: US/10/741,657A
;  CURRENT FILING DATE:  2003-12-19
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Mus sp.
US-10-741-657A-16

  Query Match             86.4%;  Score 494;  DB 17;  Length 107;
  Best Local Similarity   87.9%;  Pred. No. 4.6e-38;
  Matches   94;  Conservative    3;  Mismatches   10;  Indels    0;  Gaps    0;

Qy           1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
               ||||||| ||| |||||||||||| |||||||||||||||||||||||:|:|||||||||
Db           1 DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSNLHSGVPS 60

Qy          61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIK 107
               |||| ||| |||||| ||| |||||||| | : |||||||||||||
Db          61 RFSGSGSGADYSLTIGNLEQEDIATYFCQQGNTLPWTFGGGTKLEIK 107


RESULT 13
US-10-473-977-69
; Sequence 69, Application US/10473977
; Publication No. US20040253233A1
; GENERAL INFORMATION:
;  APPLICANT: MATEO DE ACOSTA DEL RIO, Cristina M. et al
;  TITLE OF INVENTION: GANGLIOSIDE-ASSOCIATED RECOMBINANT ANTIBODIES AND THE USE THEREO
;  TITLE OF INVENTION:  DIAGNOSIS AND TREATMENT OF TUMORS
;  FILE REFERENCE: 4565-0107P
;  CURRENT APPLICATION NUMBER: US/10/473,977
;  CURRENT FILING DATE:  2003-10-03
;  PRIOR APPLICATION NUMBER: PCT/CU02/00003
;  PRIOR FILING DATE: 2002-04-06
;  PRIOR APPLICATION NUMBER: CU 84/2001
;  PRIOR FILING DATE: 2001-04-06
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 69
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: DOMAIN
;   LOCATION: (1)..(107)
US-10-473-977-69

  Query Match             85.8%;  Score 491;  DB 17;  Length 107;
  Best Local Similarity   87.9%;  Pred. No. 8.8e-38;
  Matches   94;  Conservative    3;  Mismatches   10;  Indels    0;  Gaps    0;
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Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||| ||| |||||||||||| |||||||||||||||||||||||:|:| |||||||
Db          1 DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 60

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIK 107
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Db         61 RFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPWTFGGGTKLESK 107


RESULT 14
US-10-411-037-52
; Sequence 52, Application US/10411037
; Publication No. US20040043446A1
; GENERAL INFORMATION:
;  APPLICANT: Neose Technologies, Inc.
;  APPLICANT:  DeFrees, Shawn
;  APPLICANT:  Zopf, David
;  APPLICANT:  Bayer, Robert
;  APPLICANT:  Hakes, David
;  APPLICANT:  Chen, Xi
;  APPLICANT:  Bowe, Caryn
;  TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
;  TITLE OF INVENTION:  GALACTOSIDASE A
;  FILE REFERENCE: 040853-01-5082
;  CURRENT APPLICATION NUMBER: US/10/411,037
;  CURRENT FILING DATE:  2003-04-09
;  PRIOR APPLICATION NUMBER: US 60/328,523
;  PRIOR FILING DATE: 2001-10-10
;  PRIOR APPLICATION NUMBER: US 60/344,692
;  PRIOR FILING DATE: 2001-10-19
;  PRIOR APPLICATION NUMBER: US 60/387,292
;  PRIOR FILING DATE: 2002-06-07
;  PRIOR APPLICATION NUMBER: US 60/391,777
;  PRIOR FILING DATE: 2002-06-25
;  PRIOR APPLICATION NUMBER: US 60/396,594
;  PRIOR FILING DATE: 2002-07-17
;  PRIOR APPLICATION NUMBER: US 60/404,249
;  PRIOR FILING DATE: 2002-08-16
;  PRIOR APPLICATION NUMBER: US 60/407,527
;  PRIOR FILING DATE: 2002-08-28
;  NUMBER OF SEQ ID NOS: 75
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-411-037-52

  Query Match             85.3%;  Score 488;  DB 15;  Length 107;
  Best Local Similarity   86.9%;  Pred. No. 1.7e-37;
  Matches   93;  Conservative    4;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||| ||| |||||||||||| |||||:|||||||||||| |||||:|:| |||||||
Db          1 DIQMTQTTSSLSASLGDRVTISCRASQDINNYLNWYQQKPDGIVKLLIYYTSTLHSGVPS 60

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIK 107
              |||| |||||||||||||| |||||||| | : ||||||||||||||
Db         61 RFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPWTFGGGTKLEIK 107


RESULT 15
US-10-411-026-52
; Sequence 52, Application US/10411026
; Publication No. US20040063911A1
; GENERAL INFORMATION:
;  APPLICANT: Neose Technologies, Inc.
;  APPLICANT:  DeFrees, Shawn
;  APPLICANT:  Zopf, David
;  APPLICANT:  Bayer, Robert
;  APPLICANT:  Hakes, David
;  APPLICANT:  Chen, Xi
;  TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
;  TITLE OF INVENTION:  METHODS
;  FILE REFERENCE: 040853-01-5053
;  CURRENT APPLICATION NUMBER: US/10/411,026
;  CURRENT FILING DATE:  2003-04-09
;  PRIOR APPLICATION NUMBER: US 60/328,523
;  PRIOR FILING DATE: 2001-10-10
;  PRIOR APPLICATION NUMBER: US 60/344,692
;  PRIOR FILING DATE: 2001-10-19
;  PRIOR APPLICATION NUMBER: US 60/387,292
;  PRIOR FILING DATE: 2002-06-07
;  PRIOR APPLICATION NUMBER: US 60/391,777
;  PRIOR FILING DATE: 2002-06-25
;  PRIOR APPLICATION NUMBER: US 60/396,594
;  PRIOR FILING DATE: 2002-07-17
;  PRIOR APPLICATION NUMBER: US 60/404,249
;  PRIOR FILING DATE: 2002-08-16
;  PRIOR APPLICATION NUMBER: US 60/407,527
;  PRIOR FILING DATE: 2002-08-28
;  NUMBER OF SEQ ID NOS: 75
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-411-026-52

  Query Match             85.3%;  Score 488;  DB 15;  Length 107;
  Best Local Similarity   86.9%;  Pred. No. 1.7e-37;
  Matches   93;  Conservative    4;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||| ||| |||||||||||| |||||:|||||||||||| |||||:|:| |||||||
Db          1 DIQMTQTTSSLSASLGDRVTISCRASQDINNYLNWYQQKPDGIVKLLIYYTSTLHSGVPS 60

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIK 107
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Db         61 RFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPWTFGGGTKLEIK 107


Search completed: December 23, 2004, 19:35:50
Job time : 26.5684 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2004, 18:46:03 ; Search time 5.83589 Seconds
(without alignments)
1780.604 Million cell updates/sec

Title: US-10-089-500-56
Perfect score: 572
Sequence: 1 DIQMTQTASSLPASLGDRVT.....HQYSKLPWTFGGGTKLEIKR 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	520	90.9	111	2	A38740	Ig kappa chain V r
2	514	89.9	111	2	E38740	Ig kappa chain V r
3	510	89.2	111	2	C38740	Ig kappa chain V r
4	507	88.6	107	2	B49026	Ig kappa chain V r
5	502	87.8	108	2	S69900	Ig kappa chain (cl
6	502	87.8	111	2	G38740	Ig kappa chain V r
7	498	87.1	108	1	KVMS73	Ig kappa chain V r
8	495	86.5	122	2	A29380	Ig kappa chain pre
9	493	86.2	108	2	S69903	Ig kappa chain (cl
10	493	86.2	115	2	JL0080	Ig kappa chain pre
11	489	85.5	108	1	KVMSAR	Ig kappa chain V r
12	488	85.3	109	2	PH0888	Ig kappa chain V r
13	488	85.3	126	2	A34904	Ig kappa chain pre
14	485.5	84.9	108	2	S38862	Ig kappa chain V r
15	485	84.8	128	2	A26406	Ig kappa chain V r
16	484.5	84.7	107	2	S69901	Ig kappa chain (cl
17	481	84.1	107	2	A48677	Ig kappa chain V-J
18	481	84.1	108	2	S69902	Ig kappa chain (cl
19	480	83.9	108	2	S19970	Ig kappa chain V r
20	478	83.6	107	2	B48677	Ig kappa chain V-J
21	478	83.6	107	2	B28044	Ig kappa chain V r
22	475	83.0	107	2	A28044	Ig kappa chain V r
23	475	83.0	127	2	PH1224	Ig kappa chain pre
24	474	82.9	107	2	D48677	Ig kappa chain V-J
25	474	82.9	108	2	B26405	Ig kappa chain V r
26	473	82.7	108	2	PL0282	Ig kappa chain V r
27	473	82.7	108	2	C26405	Ig kappa chain V r
28	471.5	82.4	107	2	S69906	Ig kappa chain (cl
29	468	81.8	107	2	S32188	Ig kappa chain V r
30	466	81.5	105	2	PH0087	Ig kappa chain V r
31	462	80.8	107	2	C48677	Ig light chain V-J
32	461	80.6	108	2	S11124	Ig kappa chain V r
33	447	78.1	108	2	B30551	Ig kappa chain V r
34	429	75.0	115	2	A53276	Ig kappa chain V r
35	426	74.5	108	1	K1HUAU	Ig kappa chain V-I
36	421	73.6	93	2	S38564	Ig kappa chain V r
37	419	73.3	129	2	S52789	Ig kappa chain V r
38	408	71.3	108	1	K1HURE	Ig kappa chain V-I
39	408	71.3	127	2	S40367	Ig kappa chain V-J
40	402	70.3	108	2	B49047	Ig kappa chain V r
41	402	70.3	110	2	S44118	Ig kappa chain V-J
42	400	69.9	108	1	K1HUAG	Ig kappa chain V-I
43	399	69.8	108	1	K1HURY	Ig kappa chain V-I
44	399	69.8	131	2	S40352	Ig kappa chain V-J
45	396	69.2	108	2	S19674	Ig kappa chain V r

ALIGNMENTS

RESULT 1
A38740
Ig kappa chain V region (Py20) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004
C;Accession: A38740
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequences and antibody properties of ant
A;Reference number: A38740; MUID:91177923; PMID:1706720
A;Accession: A38740
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr
A;Molecule type: mRNA
A;Residues: 1-111 <RUF>
A;Cross-references: UNIPROT:Q91WS9
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-93/Domain: immunoglobulin homology <IMM>

Query Match 90.9%; Score 520; DB 2; Length 111;
Best Local Similarity 88.9%; Pred. No. 1.1e-40;
Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

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Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
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Db          4 DVQMTQTTSSLSASLGDRVTISCSASQGISNYLNWYQQKPDGTVKLLIYYTSSLHSGVPS 63

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              |||| ||||||||||||||||:|||:| ||||:|||||||||||||||
Db         64 RFSGSGSGTDYSLTISNLEPEDVATYYCQQYSKVPWTFGGGTKLEIKR 111
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RESULT 2
E38740
Ig kappa chain V region (Py54) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004
C;Accession: E38740
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequences and antibody properties of ant
A;Reference number: A38740; MUID:91177923; PMID:1706720
A;Accession: E38740
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr
A;Molecule type: mRNA
A;Residues: 1-111 <RUF>
A;Cross-references: UNIPROT:Q91WS9
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-93/Domain: immunoglobulin homology <IMM>

Query Match 89.9%; Score 514; DB 2; Length 111;

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  Best Local Similarity   88.9%;  Pred. No. 3.9e-40;
  Matches   96;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              |: |||| ||| |||||||||||||| ||||||||||||||||||||:|:|:|||||||
Db          4 DVMMTQTTSSLSASLGDRVTISCSASQGISNYLNWYQQKPDGTVKLLIYYTSSLHSGVPS 63

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              |||| |||||||||||:|||||||||:| ||||||||||||||||||
Db         64 RFSGSGSGTDYSLTISDLEPEDIATYYCQQYSKLPWTFGGGTKLEIKR 111


RESULT 3
C38740
Ig kappa chain V region (Py2) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004
C;Accession: C38740
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequences and antibody properties of anti
A;Reference number: A38740; MUID:91177923; PMID:1706720
A;Accession: C38740
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: mRNA
A;Residues: 1-111 <RUF>
A;Cross-references: UNIPROT:Q91WS9
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-93/Domain: immunoglobulin homology <IMM>

  Query Match             89.2%;  Score 510;  DB 2;  Length 111;
  Best Local Similarity   87.0%;  Pred. No. 9.1e-40;
  Matches   94;  Conservative    7;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              |: |||| ||| |||||||||||||| |||||||| ||||||||||:|:|:|||||||
Db          4 DVMMTQTTSSLSASLGDRVTISCSASQGISNYLNWYQHKPDGTVKLLIYYTSSLHSGVPS 63

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              |||| |||||||||||||||:|||:| ||||:|||||||||||||||
Db         64 RFSGSGSGTDYSLTISNLEPEDVATYYCQQYSKVPWTFGGGTKLEIKR 111


RESULT 4
B49026
Ig kappa chain V region, anti-idiotypic monoclonal antibody - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Accession: B49026; PL0220
R;Koizumi, T.; Puccetti, A.; Migliorini, P.; Barrett, K.J.; Schwartz, R.S.
Eur. J. Immunol. 21, 2185-2193, 1991
A;Title: Molecular heterogeneity of auto-anti-idiotypic antibodies in MLR-lpr/lpr mice.
A;Reference number: A49026; MUID:91364791; PMID:1909645
A;Accession: B49026
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-107 <KOI>
A;Experimental source: MLR-lpr/lpr
A;Note: sequence extracted from NCBI backbone (NCBIP:60876)
R;Puccetti, A.; Koizumi, T.; Migliorini, P.; Andre-Schwartz, J.; Barrett, K.J.; Schwartz
J. Exp. Med. 171, 1919-1930, 1990
A;Title: An immunoglobulin light chain from a lupus-prone mouse induces autoantibodies i
A;Reference number: PL0220; MUID:90278348; PMID:1693654
A;Accession: PL0220
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-107 <PUC>
A;Experimental source: strain lupus-prone MRL-lpr/lpr mouse
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;50-56/Region: complementarity-determining 2
F;89-97/Region: complementarity-determining 3

  Query Match             88.6%;  Score 507;  DB 2;  Length 107;
  Best Local Similarity   90.7%;  Pred. No. 1.6e-39;
  Matches   97;  Conservative    3;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||| ||| |||||||||| |||||||||||||||||||||:|:| |||||||
Db          1 DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 60

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIK 107
              |||| ||||||||||||||||||:| |||||| ||||||||||
Db         61 RFSGSGSGTDYSLTISNLEPEDIATYYCQQYSKLPRTFGGGTKLEIK 107


RESULT 5
S69900
Ig kappa chain (clone KL2.18 / KL4B10 / KL4C11) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C;Accession: S69900; S69907; S69908
R;Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.
Immunology 75, 116-121, 1992
A;Title: B-cell proliferation initiated by Ia cross-linking and sustained by interleukin
A;Reference number: S69900; MUID:92165291; PMID:1537587
A;Accession: S69900
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-108 <WYS>
A;Cross-references: EMBL:X55041; NID:g511023; PIDN:CAA38881.1; PID:g511024
A;Accession: S69907
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-108 <WY2>
A;Cross-references: EMBL:X55048; NID:g511037; PIDN:CAA38888.1; PID:g511038
A;Accession: S69908
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-108 <WY3>
A;Cross-references: EMBL:X55049; NID:g511039; PIDN:CAA38889.1; PID:g511040
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

  Query Match             87.8%;  Score 502;  DB 2;  Length 108;
  Best Local Similarity   88.9%;  Pred. No. 4.7e-39;
  Matches   96;  Conservative    3;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||| ||| |||||||||| |||||||||||||||||||||:|:| |||||||
Db          1 DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 60

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              |||| |||||||||||||| |||||||| | : |||||||||||||||
Db         61 RFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPWTFGGGTKLEIKR 108


RESULT 6
G38740
Ig kappa chain V region (Py69) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004
C;Accession: G38740
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequences and antibody properties of anti
A;Reference number: A38740; MUID:91177923; PMID:1706720
A;Accession: G38740
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: mRNA
A;Residues: 1-111 <RUF>
A;Cross-references: UNIPROT:Q91WS9
C;Superfamily: immunoglobulin V region; immunoglobulin homology
```

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C;Keywords: heterotetramer; immunoglobulin
F;19-93/Domain: immunoglobulin homology <IMM>

  Query Match             87.8%;  Score 502;  DB 2;  Length 111;
  Best Local Similarity   87.0%;  Pred. No. 4.9e-39;
  Matches   94;  Conservative    7;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              |: |||: ||| |||||||||||||||| ||||||||||||||||||:|:|:||| |||
Db          4 DVLMTQSTSSLSASLGDRVTISCSASQDIRNYLNWYQQKPDGTVKLLIYYTSSLHSEVPS 63

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              |||| ||||||||||:|||||||||:| ||||||||||||||||||||
Db         64 RFSGSGSGTDYSLTISDLEPEDIATYYCQQYSKLPWTFGGGTKLEIKR 111


RESULT 7
KVMS73
Ig kappa chain V region (MOPC 173) - mouse (tentative sequence)
C;Species: Mus musculus (house mouse)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C;Accession: A01926
R;Schiff, C.; Fougereau, M.
Eur. J. Biochem. 59, 525-537, 1975
A;Title: Determination of the primary structure of a mouse IgG2a immunoglobulin. Amino-a
A;Reference number: A01926; MUID:76091934; PMID:812696
A;Accession: A01926
A;Molecule type: protein
A;Residues: 1-108 <SCH>
A;Cross-references: UNIPROT:P01643
C;Comment: This chain was isolated from a myeloma protein.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status predicted

  Query Match             87.1%;  Score 498;  DB 1;  Length 108;
  Best Local Similarity   85.2%;  Pred. No. 1.1e-38;
  Matches   92;  Conservative    9;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||| ||| |||||||||||||| | |||:|||||||||||||:|:|:|||||||
Db          1 DIQMTQTTSSLSASLGDRVTISCSASQSIGNYLBWYQQKPDGTVKLLIYYTSSLHSGVPS 60

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              |||| ||||||||||:|:|::||||:| |||||| ||||||||||||
Db         61 RFSGSGSGTDYSLTISBLZPZBIATYYCQQYSKLPRTFGGGTKLEIKR 108


RESULT 8
A29380
Ig kappa chain precursor V region (AC-1001) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 21-Jan-2000
C;Accession: A29380
R;Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.
J. Biol. Chem. 262, 13579-13583, 1987
A;Title: Nucleotide and translated amino acid sequences of cDNA coding for the variable
A;Reference number: A92612; MUID:88007582; PMID:3115981
A;Accession: A29380
A;Molecule type: mRNA
A;Residues: 1-122 <CHE>
A;Cross-references: GB:M17160; GB:J02815; NID:g196895; PIDN:AAA38824.1; PID:g196896
A;Note: the authors translated the codon TTC for residue 1 as Leu
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;30-104/Domain: immunoglobulin homology <IMM>

  Query Match             86.5%;  Score 495;  DB 2;  Length 122;
  Best Local Similarity   88.0%;  Pred. No. 2.4e-38;
  Matches   95;  Conservative    3;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||| ||| |||||||||||| |||||:|||||||||||||||||| |:| |||||||
Db         15 DIQMTQTTSSLSASLGDRVTISCRASQDINNYLNWYQQKPDGTVKLLIHYTSRLHSGVPS 74

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              |||| |||||||||||||| |||||||| | : |||||||||||||||
Db         75 RFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPWTFGGGTKLEIKR 122


RESULT 9
S69903
Ig kappa chain (clone KL2.29 / KL2.33 / KL3.8) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C;Accession: S69903; S69904; S69905
R;Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.
Immunology 75, 116-121, 1992
A;Title: B-cell proliferation initiated by Ia cross-linking and sustained by interleuki
A;Reference number: S69900; MUID:92165291; PMID:1537587
A;Accession: S69903
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-108 <WYS>
A;Cross-references: EMBL:X55044; NID:g511029; PIDN:CAA38884.1; PID:g511030
A;Accession: S69904
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-108 <WY2>
A;Cross-references: EMBL:X55045; NID:g511031; PIDN:CAA38885.1; PID:g511032
A;Accession: S69905
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-108 <WY3>
A;Cross-references: EMBL:X55046; NID:g511033; PIDN:CAA38886.1; PID:g511034
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

  Query Match             86.2%;  Score 493;  DB 2;  Length 108;
  Best Local Similarity   88.0%;  Pred. No. 3.1e-38;
  Matches   95;  Conservative    4;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||| ||| |||||||||||| |||||||||||||||||||||:|:| |||||||
Db          1 DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 60

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              |||| |||||||||||||| |||||||| | : ||:|||||||||||
Db         61 RFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGTKLEIKR 108


RESULT 10
JL0080
Ig kappa chain precursor V region (anti-phenyloxazolone, 18C10) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jan-2000
C;Accession: JL0080
R;Kaartinen, M.; Rocca-Serra, J.; Maekelae, O.
Mol. Immunol. 25, 859-865, 1988
A;Title: Combinatorial association of V genes: one VH gene codes for three non-cross-re
A;Reference number: JL0076; MUID:89096973; PMID:3211160
A;Accession: JL0080
A;Molecule type: mRNA
A;Residues: 1-115 <KAA>
A;Cross-references: GB:M27793; NID:g197161; PIDN:AAA38937.1; PID:g197162
A;Note: the authors translated the codon AGG for residue 30 as Ser
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-6/Domain: signal sequence (fragment) #status predicted <SIG>
F;7-115/Product: Ig light chain #status predicted <MAT>
F;22-96/Domain: immunoglobulin homology <IMM>
F;30-40/Region: complementarity-determining 1
F;56-62/Region: complementarity-determining 2
```

```
  Query Match             86.2%;  Score 493;  DB 2;  Length 115;
  Best Local Similarity   88.0%;  Pred. No. 3.4e-38;
  Matches   95;  Conservative    4;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||| ||| |||||||||| |||||||||||||||||||||||:|:| |||||||
Db          7 DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 66

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              |||| |||||||||||||| |||||||| | : ||:||||||||||||
Db         67 RFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGTKLEIKR 114


RESULT 11
KVMSAR
Ig kappa chain V regions (anti-arsonate hybridoma proteins) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jul-1982 #sequence_revision 06-Jul-1982 #text_change 09-Jul-2004
C;Accession: A01927
R;Siegelman, M.; Capra, J.D.
Proc. Natl. Acad. Sci. U.S.A. 78, 7679-7683, 1981
A;Title: Complete amino acid sequence of light chain variable regions derived from five
A;Reference number: A01927; MUID:82150934; PMID:6801658
A;Accession: A01927
A;Molecule type: protein
A;Residues: 1-108 <SIE>
A;Cross-references: UNIPROT:P01644
A;Experimental source: strain A/J
A;Note: hP 93G7 differs in having 93-Met; HP 123E6 differs in having 7-Ser, 92-Tyr, and
Arg, 84-Ser, and 93-Ala
C;Comment: The sequence shown is HP R16.7.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status predicted

  Query Match             85.5%;  Score 489;  DB 1;  Length 108;
  Best Local Similarity   88.0%;  Pred. No. 7.3e-38;
  Matches   95;  Conservative    3;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||| ||| |||||||||| |||||||||||||||||||||||:|:| |||||||
Db          1 DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 60

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              |||| |||||||||||||| |||||||| | : || ||||||||||||
Db         61 RFSGSGSGTDYSLTISNLEQEDIATYFCQQGNSLPRTFGGGTKLEIKR 108


RESULT 12
PH0888
Ig kappa chain V region (anti-CD3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000
C;Accession: PH0888
R;Shalaby, M.R.; Shepard, H.M.; Presta, L.; Rodrigues, M.L.; Beverley, P.C.L.; Feldmann,
J. Exp. Med. 175, 217-225, 1992
A;Title: Development of humanized bispecific antibodies reactive with cytotoxic lymphocy
A;Reference number: PH0885; MUID:92113462; PMID:1346155
A;Accession: PH0888
A;Molecule type: mRNA
A;Residues: 1-109 <SHA>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

  Query Match             85.3%;  Score 488;  DB 2;  Length 109;
  Best Local Similarity   86.1%;  Pred. No. 9.1e-38;
  Matches   93;  Conservative    4;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||| ||| |||||||||| |||||||||||||||||||||||:|:| |||||||
Db          1 DIQMTQTTSSLSASLGDRVTISCRASQDIRNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 60

Qy         61 RFSGGGSGTDYSLTISNLEQEDIATYFCQQGNTLPWTFAGGTKLEIKR 108
              :||| |||||||||||||| |||||||| | : ||||| |||||||||
Db         61 KFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPWTFAGGTKLEIKR 108


RESULT 13
A34904
Ig kappa chain precursor V region (5-27) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 09-Jul-2004
C;Accession: A34904
R;Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
A;Title: Active site structure and antigen binding properties of idiotypically cross-rea
A;Reference number: A34903; MUID:90094387; PMID:2104617
A;Accession: A34904
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-126 <BED>
A;Cross-references: UNIPROT:Q91WF8
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;35-109/Domain: immunoglobulin homology <IMM>

  Query Match             85.3%;  Score 488;  DB 2;  Length 126;
  Best Local Similarity   86.8%;  Pred. No. 1.1e-37;
  Matches   92;  Conservative    5;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||| ||| ||||||||:|| |||||:||||||||||||||||:|:| |||||||
Db         20 DIQMTQTTSSLSASLGDRVTVSCRASQDINNYLNWYQQKPDGTVKLLIYYTSKLHSGVPS 79

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEI 106
              |||| |||||||||||||| |||||||| | : ||||||||||||
Db         80 RFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPWTFGGGTKLEI 125


RESULT 14
S38862
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C;Accession: S38862
R;Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F.
submitted to the EMBL Data Library, August 1993
A;Description: Production and cloning of TMV-specific monoclonal antibodies.
A;Reference number: S37200
A;Accession: S38862
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-108 <FIS>
A;Cross-references: EMBL:X75854; NID:g429109; PID:g429110
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

  Query Match             84.9%;  Score 485.5;  DB 2;  Length 108;
  Best Local Similarity   87.0%;  Pred. No. 1.5e-37;
  Matches   94;  Conservative    4;  Mismatches    9;  Indels    1;  Gaps    1;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              |:||||| ||| |||||||||| |||||||||||||||||||||||:|:| |||||||
Db          1 DVQMTQTTSSLAASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 60

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKL-PWTFGGGTKLEIK 107
              |||| |||||||||||||| |||||||| | : | ||||||||||||
Db         61 RFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPPWTFGGGTKLEIK 108
```

RESULT 15
A26406
Ig kappa chain V region (Ars-A) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C;Accession: A26406
R;Sanz, I.; Capra, J.D.
Proc. Natl. Acad. Sci. U.S.A. 84, 1085-1089, 1987
A;Title: V-K and J-K gene segments of A/J Ars-A antibodies: somatic recombination genera
A;Reference number: A26406; MUID:87147197; PMID:3103124
A;Accession: A26406
A;Molecule type: DNA
A;Residues: 1-128 <SAN>
A;Cross-references: UNIPROT:Q91WF8; GB:M15519
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

Query Match 84.8%; Score 485; DB 2; Length 128;
Best Local Similarity 87.0%; Pred. No. 2e-37;
Matches 94; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

```
Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||| ||| |||||||||| |||||||||||||||||||||:|:| |||||||
Db         21 DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 80

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              |||| |||||||||||||| |||:|||| | : || ||||||||||||
Db         81 RFSGSGSGTDYSLTISNLEQEDISTYFCQQGNALPRTFGGGTKLEIKR 128
```

Search completed: December 23, 2004, 19:06:06
Job time : 5.83589 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2004, 18:31:20 ; Search time 30.044 Seconds
(without alignments)
2068.313 Million cell updates/sec

Title: US-10-089-500-56
Perfect score: 572
Sequence: 1 DIQMTQTASSLPASLGDRVT.....HQYSKLPWTFGGGTKLEIKR 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	506	88.5	233	2	Q91WS9	Q91ws9 mus musculu
2	498	87.1	108	1	KV5J_MOUSE	P01643 mus musculu
3	494	86.4	234	2	Q8R062	Q8r062 mus musculu
4	489	85.5	108	1	KV5K_MOUSE	P01644 mus musculu
5	488	85.3	108	1	KV5L_MOUSE	P01645 mus musculu
6	486	85.0	111	2	AAR10992	Aar10992 mus muscu
7	484	84.6	108	1	KV5N_MOUSE	P01647 mus musculu
8	481	84.1	108	1	KV5M_MOUSE	P01646 mus musculu
9	477	83.4	108	1	KV5O_MOUSE	P01648 mus musculu
10	466	81.5	234	2	Q91WF8	Q91wf8 mus musculu
11	460	80.4	107	2	Q9JL84	Q9jl84 mus musculu
12	458	80.1	108	1	KV5U_MOUSE	P04946 mus musculu
13	457	79.9	103	2	AAR11052	Aar11052 mus muscu
14	437	76.4	104	2	AAR11043	Aar11043 mus muscu
15	436	76.2	104	2	AAR11000	Aar11000 mus muscu
16	426	74.5	108	1	KV1B_HUMAN	P01594 homo sapien
17	408	71.3	108	1	KV1O_HUMAN	P01607 homo sapien
18	401	70.1	108	1	KV1Y_HUMAN	P80362 homo sapien
19	400	69.9	108	1	KV1A_HUMAN	P01593 homo sapien
20	399	69.8	108	1	KV1P_HUMAN	P01608 homo sapien
21	396	69.2	108	2	Q9UL70	Q9ul70 homo sapien
22	394.5	69.0	107	2	Q96SA9	Q96sa9 homo sapien
23	394	68.9	108	2	Q9UL77	Q9ul77 homo sapien
24	394	68.9	130	1	KV5G_MOUSE	P01639 mus musculu
25	394	68.9	236	2	Q6GMX9	Q6gmx9 homo sapien
26	386	67.5	236	2	Q6GMX0	Q6gmx0 homo sapien
27	385	67.3	108	1	KV1R_HUMAN	P01610 homo sapien
28	385	67.3	236	2	Q6GMW1	Q6gmw1 homo sapien
29	383	67.0	108	1	KV1L_HUMAN	P01604 homo sapien
30	382	66.8	236	2	Q7Z3Y4	Q7z3y4 homo sapien
31	380	66.4	108	1	KV1M_HUMAN	P01605 homo sapien
32	380	66.4	236	2	Q7TMK3	Q7tmk3 mus musculu
33	379	66.3	236	2	Q6GMX8	Q6gmx8 homo sapien
34	377	65.9	108	1	KV5P_MOUSE	P01649 mus musculu
35	375	65.6	116	2	Q96PF6	Q96pf6 homo sapien
36	375	65.6	236	2	Q6PIH7	Q6pih7 homo sapien
37	375	65.6	236	2	AAH34141	Aah34141 homo sapi
38	374	65.4	108	1	KV1C_HUMAN	P01595 homo sapien
39	374	65.4	108	1	KV1N_HUMAN	P01606 homo sapien
40	374	65.4	108	1	KV1S_HUMAN	P01611 homo sapien
41	374	65.4	129	1	KV1W_HUMAN	P04431 homo sapien
42	371.5	64.9	107	2	Q9UL81	Q9ul81 homo sapien
43	370	64.7	108	1	KV1H_HUMAN	P01600 homo sapien
44	370	64.7	108	1	KV1K_HUMAN	P01603 homo sapien
45	370	64.7	236	2	Q7TS98	Q7ts98 mus musculu

ALIGNMENTS

```
RESULT 1
Q91WS9
ID   Q91WS9      PRELIMINARY;      PRT;   233 AA.
AC   Q91WS9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Colon;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Colon;
RA   Strausberg R.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC013496; AAH13496.1; -.
DR   PIR; A38740; A38740.
DR   PIR; C38740; C38740.
DR   PIR; E38740; E38740.
DR   PIR; G38740; G38740.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
```

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DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
FT   NON_TER      1      1
SQ   SEQUENCE   233 AA;  25781 MW;  B1C184DA149A16EB CRC64;

  Query Match             88.5%;  Score 506;  DB 2;  Length 233;
  Best Local Similarity   88.0%;  Pred. No. 2.4e-43;
  Matches   95;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||| ||| |||||||||||| || |:|||||||||||||||||:|:|:|||||||
Db         20 DIQMTQTTSSLSASLGDRVTISCSGSQGIANYLNWYQQKPDGTVKLLIYYTSSLHSGVPS 79

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              |||| ||||||||||||||||||||:| ||   ||||||||||||||
Db         80 RFSGSGSGTDYSLTISNLEPEDIATYYCQQYRYLPWTFGGGTKLEIKR 127


RESULT 2
KV5J_MOUSE
ID   KV5J_MOUSE     STANDARD;      PRT;   108 AA.
AC   P01643;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig kappa chain V-V region MOPC 173.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=76091934; PubMed=812696;
RA   Schiff C., Fougereau M.;
RT   "Determination of the primary structure of a mouse IgG2a
RT   immunoglobulin. Amino-acid sequence of the light chain.";
RL   Eur. J. Biochem. 59:525-537(1975).
CC   -!- MISCELLANEOUS: This chain was isolated from a myeloma protein.
DR   PIR; A01926; KVMS73.
DR   HSSP; P01594; 1JV5.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region.
FT   DOMAIN        1     23       Framework-1.
FT   DOMAIN       24     34       Complementarity-determining-1.
FT   DOMAIN       35     49       Framework-2.
FT   DOMAIN       50     56       Complementarity-determining-2.
FT   DOMAIN       57     88       Framework-3.
FT   DOMAIN       89     97       Complementarity-determining-3.
FT   DOMAIN       98    108       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11819 MW;  2AD29D92A72AA0A3 CRC64;

  Query Match             87.1%;  Score 498;  DB 1;  Length 108;
  Best Local Similarity   85.2%;  Pred. No. 6.6e-43;
  Matches   92;  Conservative    9;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||| ||| |||||||||||||| | |||:|||||||||||||:|:|:|||||||
Db          1 DIQMTQTTSSLSASLGDRVTISCSASQSIGNYLBWYQQKPDGTVKLLIYYTSSLHSGVPS 60

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              |||| |||||||||||:|:|::||||:| |||||| ||||||||||||
Db         61 RFSGSGSGTDYSLTISBLZPZBIATYYCQQYSKLPRTFGGGTKLEIKR 108


RESULT 3
Q8R062
ID   Q8R062      PRELIMINARY;      PRT;   234 AA.
AC   Q8R062;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Colon;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Colon;
RA   Strausberg R.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC027418; AAH27418.1; -.
DR   HSSP; P01594; 1JV5.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   234 AA;  25858 MW;  4EB08C81426AEAB1 CRC64;

  Query Match             86.4%;  Score 494;  DB 2;  Length 234;
  Best Local Similarity   87.0%;  Pred. No. 4.1e-42;
  Matches   94;  Conservative    6;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||| ||| |||||||||||||| |||||||||||||||||:|:|:|||||||
Db         21 DIQMTQTTSSLSASLGDRVTISCSASQGISNYLNWYQQKPDGTVKLLIYYTSSLHSGVPS 80

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              |||| |||| |||||||||||||||:| |||: |:||| ||||||||
Db         81 RFSGSGSGTHYSLTISNLEPEDIATYYCQQYSQFPFTFGSGTKLEIKR 128


RESULT 4
KV5K_MOUSE
ID   KV5K_MOUSE     STANDARD;      PRT;   108 AA.
AC   P01644;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig kappa chain V-V region HP R16.7.
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OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=A/J;
RX   MEDLINE=82150934; PubMed=6801658;
RA   Siegelman M., Capra J.D.;
RT   "Complete amino acid sequence of light chain variable regions derived
RT   from five monoclonal anti-p-azophenylarsonate antibodies differing
RT   with respect to a crossreactive idiotype.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC   -!- MISCELLANEOUS: Anti-arsonate hybridoma protein.
DR   PIR; A01927; KVMSAR.
DR   HSSP; P01594; 1JV5.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region.
FT   DOMAIN        1     23       Framework-1.
FT   DOMAIN       24     34       Complementarity-determining-1.
FT   DOMAIN       35     49       Framework-2.
FT   DOMAIN       50     56       Complementarity-determining-2.
FT   DOMAIN       57     88       Framework-3.
FT   DOMAIN       89     97       Complementarity-determining-3.
FT   DOMAIN       98    108       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11910 MW;  A554642C63EFF597 CRC64;

  Query Match             85.5%;  Score 489;  DB 1;  Length 108;
  Best Local Similarity   88.0%;  Pred. No. 5.4e-42;
  Matches   95;  Conservative    3;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||| ||| |||||||||| |||||||||||||||||||||||:|:| |||||||
Db          1 DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 60

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              |||| |||||||||||||| |||||||| | : || ||||||||||||
Db         61 RFSGSGSGTDYSLTISNLEQEDIATYFCQQGNSLPRTFGGGTKLEIKR 108


RESULT 5
KV5L_MOUSE
ID   KV5L_MOUSE     STANDARD;      PRT;   108 AA.
AC   P01645;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig kappa chain V-V region HP 93G7.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=A/J;
RX   MEDLINE=82150934; PubMed=6801658;
RA   Siegelman M., Capra J.D.;
RT   "Complete amino acid sequence of light chain variable regions derived
RT   from five monoclonal anti-p-azophenylarsonate antibodies differing
RT   with respect to a crossreactive idiotype.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC   -!- MISCELLANEOUS: Anti-arsonate hybridoma protein.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region.
FT   DOMAIN        1     23       Framework-1.
FT   DOMAIN       24     34       Complementarity-determining-1.
FT   DOMAIN       35     49       Framework-2.
FT   DOMAIN       50     56       Complementarity-determining-2.
FT   DOMAIN       57     88       Framework-3.
FT   DOMAIN       89     97       Complementarity-determining-3.
FT   DOMAIN       98    108       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11954 MW;  22F4642C63EFF58E CRC64;

  Query Match             85.3%;  Score 488;  DB 1;  Length 108;
  Best Local Similarity   88.0%;  Pred. No. 6.9e-42;
  Matches   95;  Conservative    3;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||| ||| |||||||||| |||||||||||||||||||||||:|:| |||||||
Db          1 DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 60

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              |||| |||||||||||||| |||||||| | : || ||||||||||||
Db         61 RFSGSGSGTDYSLTISNLEQEDIATYFCQQGNMLPRTFGGGTKLEIKR 108


RESULT 6
AAR10992
ID   AAR10992    PRELIMINARY;      PRT;   111 AA.
AC   AAR10992;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   ANA immunoglobulin kappa light chain (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=B6.Sle1; TISSUE=Spleen;
RA   Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RT   "Antinuclear autoantibodies from B6.Sle1 mice.";
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY436832; AAR10992.1; -.
FT   NON_TER       1      1
FT   NON_TER     111    111
SQ   SEQUENCE   111 AA;  12120 MW;  879A9D6B5880C59D CRC64;

  Query Match             85.0%;  Score 486;  DB 2;  Length 111;
  Best Local Similarity   88.6%;  Pred. No. 1.1e-41;
  Matches   93;  Conservative    3;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          4 MTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPSRFS 63
              |||| ||| |||||||||| |||||||||||||||||||||||:|:| ||||||||||
Db          1 MTQTPSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPSRFS 60

Qy         64 GGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              | |||||||||||||| |||||||| | : ||||||||||||||
Db         61 GSGSGTDYSLTISNLEQEDIATYFCQQGNTLPWTFGGGTKLEIKR 105


RESULT 7
KV5N_MOUSE
ID   KV5N_MOUSE     STANDARD;      PRT;   108 AA.
AC   P01647;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig kappa chain V-V region HP 124E1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=A/J;
RX   MEDLINE=82150934; PubMed=6801658;
RA   Siegelman M., Capra J.D.;
RT   "Complete amino acid sequence of light chain variable regions derived
RT   from five monoclonal anti-p-azophenylarsonate antibodies differing
RT   with respect to a crossreactive idiotype.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC   -!- MISCELLANEOUS: Anti-arsonate hybridoma protein.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region.
FT   DOMAIN        1     23       Framework-1.
FT   DOMAIN       24     34       Complementarity-determining-1.
FT   DOMAIN       35     49       Framework-2.
FT   DOMAIN       50     56       Complementarity-determining-2.
FT   DOMAIN       57     88       Framework-3.
FT   DOMAIN       89     97       Complementarity-determining-3.
FT   DOMAIN       98    108       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11965 MW;  39971BC653EFEFA2 CRC64;

  Query Match             84.6%;  Score 484;  DB 1;  Length 108;
  Best Local Similarity   87.0%;  Pred. No. 1.8e-41;
  Matches   94;  Conservative    3;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              |||||||  ||| |||||||||||  |||||:||||||||||||||||||:|:| |||||||
Db          1 DIQMTQTTSSLSASLGDRVTISCRASQDINNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 60

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              ||||  |||||||||||||| |||||||  |    || ||||||||||||
Db         61 RFSGSGSGTDYSLTISNLEQEDIATYFCQQGKTLPRTFGGGTKLEIKR 108


RESULT 8
KV5M_MOUSE
ID   KV5M_MOUSE     STANDARD;      PRT;   108 AA.
AC   P01646;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig kappa chain V-V region HP 123E6.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=A/J;
RX   MEDLINE=82150934; PubMed=6801658;
RA   Siegelman M., Capra J.D.;
RT   "Complete amino acid sequence of light chain variable regions derived
RT   from five monoclonal anti-p-azophenylarsonate antibodies differing
RT   with respect to a crossreactive idiotype.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC   -!- MISCELLANEOUS: Anti-arsonate hybridoma protein.
DR   HSSP; P01594; 1JV5.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region.
FT   DOMAIN        1     23       Framework-1.
FT   DOMAIN       24     34       Complementarity-determining-1.
FT   DOMAIN       35     49       Framework-2.
FT   DOMAIN       50     56       Complementarity-determining-2.
FT   DOMAIN       57     88       Framework-3.
FT   DOMAIN       89     97       Complementarity-determining-3.
FT   DOMAIN       98    108       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11989 MW;  4C98599C08EBA09A CRC64;

  Query Match             84.1%;  Score 481;  DB 1;  Length 108;
  Best Local Similarity   87.0%;  Pred. No. 3.5e-41;
  Matches   94;  Conservative    3;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||: ||| |||||||||||  |||||||||||||||||||||||:|:| |||||||
Db          1 DIQMTQSTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 60

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              ||||  |||||||||||||| |||||||  |    || ||||||||||||
Db         61 RFSGSGSGTDYSLTISNLEQEDIATYFCQQGYMLPRTFGGGTKLEIKR 108


RESULT 9
KV5O_MOUSE
ID   KV5O_MOUSE     STANDARD;      PRT;   108 AA.
AC   P01648;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig kappa chain V-V region HP 91A3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=A/J;
RX   MEDLINE=82150934; PubMed=6801658;
RA   Siegelman M., Capra J.D.;
RT   "Complete amino acid sequence of light chain variable regions derived
RT   from five monoclonal anti-p-azophenylarsonate antibodies differing
RT   with respect to a crossreactive idiotype.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC   -!- MISCELLANEOUS: Anti-arsonate hybridoma protein.
DR   HSSP; P01594; 1JV5.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region.
FT   DOMAIN        1     23       Framework-1.
FT   DOMAIN       24     34       Complementarity-determining-1.
FT   DOMAIN       35     49       Framework-2.
FT   DOMAIN       50     56       Complementarity-determining-2.
FT   DOMAIN       57     88       Framework-3.
FT   DOMAIN       89     97       Complementarity-determining-3.
FT   DOMAIN       98    108       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11961 MW;  D52EDA5E9A45291C CRC64;

  Query Match             83.4%;  Score 477;  DB 1;  Length 108;
  Best Local Similarity   85.2%;  Pred. No. 9.1e-41;
  Matches   92;  Conservative    6;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              |||||||  ||| |||||||||||  |||||:||||||:|||||||||||:|:| |||||||
Db          1 DIQMTQTPSSLSASLGDRVTISCRASQDINNYLNWYRQKPDGTVKLLIYYTSRLHSGVPS 60

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              ||||  |||||||||||||| |||:|||| | : || ||||||||||||
Db         61 RFSGSGSGTDYSLTISNLEQEDISTYFCQQGNALPRTFGGGTKLEIKR 108
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RESULT 10
Q91WF8
ID   Q91WF8      PRELIMINARY;      PRT;   234 AA.
AC   Q91WF8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Colon;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Colon;
RA   Strausberg R.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC015292; AAH15292.1; -.
DR   PIR; A26406; A26406.
DR   PIR; A34904; A34904.
DR   PDB; 1JFQ; X-ray; L=21-234.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   InterPro; IPR001865; Ribosomal_S2.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR   PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   234 AA;  25929 MW;  B0D0B0E6EB7812D2 CRC64;

  Query Match            81.5%;  Score 466;  DB 2;  Length 234;
  Best Local Similarity  83.3%;  Pred. No. 2.9e-39;
  Matches   90;  Conservative    6;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||| ||| |||||||||||| |||||||||||||||||||||||:|:| |: ||||
Db         21 DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLYLGVPS 80

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              |||| ||||||||||||| |||||||| | :  |:||| |||||:||
Db         81 RFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTPPFTFGSGTKLEVKR 128

RESULT 11
Q9JL84
ID   Q9JL84      PRELIMINARY;      PRT;   107 AA.
AC   Q9JL84;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Anti-myosin immunoglobulin light chain variable region
DE   (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RX   MEDLINE=20448942; PubMed=10992488;
RA   Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT   "T-Cell-dependent antibody response to the dominant epitope of
RT   streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT   with cardiac myosin.";
RL   Infect. Immun. 68:5803-5808(2000).
DR   EMBL; AF206022; AAF69320.1; -.
DR   HSSP; P01594; 1JV5.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     107    107
SQ   SEQUENCE   107 AA;  11648 MW;  ACF9B1253ACA1E5D CRC64;

  Query Match            80.4%;  Score 460;  DB 2;  Length 107;
  Best Local Similarity  81.3%;  Pred. No. 4.9e-39;
  Matches   87;  Conservative    6;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||: ||| ||||||| |||| ||| |:|||||||||||||:|:|:| |||||
Db          1 DIQMTQSTSSLSASLGDRVXXXCSASQGISNXXXWFQQKPDGTVKLLIYYTSSLXSGVPS 60

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIK 107
              |||| ||| ||||||||||||||||:| |||| ||||||||||||
Db         61 RFSGSGSGXDYSLTISNLEPEDIATYYCQQYSKFPWTFGGGTKLEIK 107


RESULT 12
KV5U_MOUSE
ID   KV5U_MOUSE     STANDARD;      PRT;   108 AA.
AC   P04946;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   29-MAR-2004 (Rel. 43, Last annotation update)
DE   Ig kappa chain V-V region NQ5-89.4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83271467; PubMed=6877353;
RA   Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT   "mRNA sequences define an unusually restricted IgG response to 2-
RT   phenyloxazolone and its early diversification.";
RL   Nature 304:320-324(1983).
CC   -!- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; K00745; AAA38690.1; -.
DR   HSSP; P01594; 1JV5.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Hybridoma; Immunoglobulin V region.
FT   DOMAIN        1     23       Framework-1.
FT   DOMAIN       24     34       Complementarity-determining-1.
FT   DOMAIN       35     49       Framework-2.
FT   DOMAIN       50     56       Complementarity-determining-2.
FT   DOMAIN       57     88       Framework-3.
FT   DOMAIN       89     97       Complementarity-determining-3.
FT   DOMAIN       98    107       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11866 MW;  DB2C885920DC6DDD CRC64;

  Query Match             80.1%;  Score 458;  DB 1;  Length 108;
  Best Local Similarity   81.5%;  Pred. No. 7.8e-39;
  Matches   88;  Conservative    7;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPS 60
              ||||||| ||| |||| ||||:||||||||||||||||||||||||:|:| |||||||
Db          1 DIQMTQTTSSLSASLGHRVTITCSASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 60

Qy         61 RFSGGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              |||| || |||||||:||: || ||| | | : ||:||||||| |||
Db         61 RFSGSGSATDYSLTITNLQQEDXATYXCQQGNTLPYTFGGGTKLXIKR 108


RESULT 13
AAR11052
ID   AAR11052    PRELIMINARY;      PRT;   103 AA.
AC   AAR11052;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   ANA immunoglobulin kappa light chain (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=B6.Sle1; TISSUE=Spleen;
RA   Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RT   "Antinuclear autoantibodies from B6.Sle1 mice.";
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY436892; AAR11052.1; -.
FT   NON_TER       1      1
FT   NON_TER     103    103
SQ   SEQUENCE   103 AA;  11332 MW;  B103B7D98711B901 CRC64;

  Query Match             79.9%;  Score 457;  DB 2;  Length 103;
  Best Local Similarity   86.3%;  Pred. No. 9.4e-39;
  Matches   88;  Conservative    3;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          4 MTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPSRFS 63
              |||| ||| |||||||||||| |||||| ||||||||||||||||:|:| ||||||||||
Db          1 MTQTPSSLSASLGDRVTISCRASQDISYYLNWYQQKPDGTVKLLIYYTSRLHSGVPSRFS 60

Qy         64 GGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLE 105
              | ||||||||||||| |||||||   : ||||||||||||
Db         61 GSGSGTDYSLTISNLEEEDIATYFCQLGNTLPWTFGGGTKLE 102


RESULT 14
AAR11043
ID   AAR11043    PRELIMINARY;      PRT;   104 AA.
AC   AAR11043;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   ANA immunoglobulin kappa light chain (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=B6.Sle1; TISSUE=Spleen;
RA   Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RT   "Antinuclear autoantibodies from B6.Sle1 mice.";
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY436883; AAR11043.1; -.
FT   NON_TER       1      1
FT   NON_TER     104    104
SQ   SEQUENCE   104 AA;  11473 MW;  58E393C037D426A7 CRC64;

  Query Match             76.4%;  Score 437;  DB 2;  Length 104;
  Best Local Similarity   82.8%;  Pred. No. 1e-36;
  Matches   82;  Conservative    6;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          4 MTQTASSLPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPSRFS 63
              |||| ||| |||||||||||| ||||||:||||:||||||||||||:|:| |||||||||
Db          1 MTQTPSSLSASLGDRVTISCRASQDISSYLNWFQQKPDGTVKLLIYYTSRLHSGVPSRFG 60

Qy         64 GGGSGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGT 102
              | |||||||||||||| || |||:| | : |||||||||
Db         61 GSGSGTDYSLTISNLEQEDFATYYCLQVNTLPWTFGGGT 99


RESULT 15
AAR11000
ID   AAR11000    PRELIMINARY;      PRT;   104 AA.
AC   AAR11000;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   ANA immunoglobulin kappa light chain (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=B6.Sle1; TISSUE=Spleen;
RA   Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RT   "Antinuclear autoantibodies from B6.Sle1 mice.";
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY436840; AAR11000.1; -.
FT   NON_TER       1      1
FT   NON_TER     104    104
SQ   SEQUENCE   104 AA;  11250 MW;  014C270D5B104DC6 CRC64;

  Query Match             76.2%;  Score 436;  DB 2;  Length 104;
  Best Local Similarity   83.7%;  Pred. No. 1.3e-36;
  Matches   82;  Conservative    7;  Mismatches    9;  Indels    0;  Gaps    0;

Qy         11 LPASLGDRVTISCSASQDISNYLNWYQQKPDGTVKLLIFYSSNLHSGVPSRFSGGGSGTD 70
              | |||||||||| | |||||||||||||||||||:::| |||||||||| |||||
Db          1 LSASLGDRVTISCRAGQDISNYLNWYQQKPDGTVKLLIYFTSKLHSGVPSRFSGSGSGTD 60

Qy         71 YSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
              :|||||||: |||||||| | : ||:|||||||||||
Db         61 FSLTISNLDQEDIATYFCQQGNSLPYTFGGGTKLEIKR 98


Search completed: December 23, 2004, 19:04:40
Job time : 31.044 secs
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2004, 18:30:04 ; Search time 155.692 Seconds
(without alignments)
1340.986 Million cell updates/sec

Title: US-10-089-500-57
Perfect score: 3071
Sequence: 1 EVTLVESGGDFVKPGGSLKV.....IVEFLNRWITFCQSIISTLT 582

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3071	100.0	582	4	AAB81991	Aab81991 Gangliosi
2	3026	98.5	582	4	AAB81987	Aab81987 Gangliosi
3	2759.5	89.9	583	4	AAB83156	Aab83156 Gangliosi
4	2744.5	89.4	579	6	AAE33444	Aae33444 KS antibo
5	2738.5	89.2	579	6	AAO30910	Aao30910 dI-KS-ala
6	2731.5	88.9	581	4	AAB81972	Aab81972 Gangliosi
7	2715.5	88.4	575	8	ADP42961	Adp42961 Humanised
8	2592	84.4	580	6	AAO30915	Aao30915 dI-NHS76
9	2560	83.4	580	6	AAO30913	Aao30913 dI-NHS76
10	2218.5	72.2	449	5	AAO18400	Aao18400 Mature hu
11	2216	72.2	713	8	ADN97491	Adn97491 Artificia
12	2216	72.2	715	8	ADN97489	Adn97489 Artificia
13	2209.5	71.9	475	7	ADM47075	Adm47075 Mouse ant
14	2205	71.8	477	2	AAR47453	Aar47453 chiT84.12
15	2203.5	71.8	471	8	ADM72029	Adm72029 Chimeric
16	2201.5	71.7	447	6	AAE33522	Aae33522 Human AQC
17	2200.5	71.7	444	6	AAE35327	Aae35327 Humanised
18	2200.5	71.7	444	6	AAE34876	Aae34876 BIWA4/8 a
19	2200.5	71.7	444	8	ADL15443	Adl15443 Humanised
20	2200.5	71.7	444	8	ADO00851	Ado00851 Humanised
21	2195.5	71.5	445	6	AAO31101	Aao31101 Human A2-
22	2195.5	71.5	447	6	AAE33523	Aae33523 Human AQC
23	2194.5	71.5	450	8	ADH34587	Adh34587 023 heavy
24	2194	71.4	449	6	ABP58273	Abp58273 Humanised
25	2194	71.4	468	6	ABP58275	Abp58275 Humanised
26	2191.5	71.4	447	6	AAE33524	Aae33524 Human AQC
27	2189.5	71.3	463	8	ADM72025	Adm72025 Chimeric
28	2187	71.2	451	8	ADH34584	Adh34584 008 heavy
29	2184.5	71.1	446	7	ADF11425	Adf11425 2D8 anti-
30	2184	71.1	451	8	ADP88494	Adp88494 Humanised
31	2181	71.0	449	3	AAY68810	Aay68810 A rat hea
32	2181	71.0	474	5	AAO14065	Aao14065 Heavy cha
33	2181	71.0	474	6	ABU08017	Abu08017 Human mon
34	2181	71.0	474	7	ADF65775	Adf65775 Human mon
35	2181	71.0	474	8	ADJ92515	Adj92515 Human SOJ
36	2180.5	71.0	461	6	ABR39847	Abr39847 Hu266 N56
37	2180.5	71.0	461	6	ABR39843	Abr39843 Hu266 N56
38	2177.5	70.9	442	6	ABR39465	Abr39465 Humanised
39	2177.5	70.9	442	6	ABU08311	Abu08311 Humanised
40	2177.5	70.9	442	6	ABB80109	Abb80109 Heavy cha
41	2177.5	70.9	442	7	ADE94066	Ade94066 Humanised
42	2177.5	70.9	442	8	ADN61714	Adn61714 Humanised
43	2177.5	70.9	461	4	AAU07745	Aau07745 Humanised
44	2177.5	70.9	461	6	ABR39844	Abr39844 Hu266 N56
45	2177.5	70.9	461	6	ABR39848	Abr39848 Hu266 N56

ALIGNMENTS

RESULT 1
AAB81991
ID AAB81991 standard; protein; 582 AA.
XX
AC AAB81991;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 57.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Claim 39; Page 175-179; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 582 AA;

Query Match 100.0%; Score 3071; DB 4; Length 582;
Best Local Similarity 100.0%; Pred. No. 4.3e-149;
Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSSA 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSSA 120

Qy        121 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180

Qy        181 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 240

Qy        241 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300

Qy        301 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360

Qy        361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 420

Qy        421 QGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMILNGINNY 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 QGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMILNGINNY 480

Qy        481 KNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINV 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 KNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINV 540

Qy        541 IVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 582
              |||||||||||||||||||||||||||||||||||||||||||
Db        541 IVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 582
```

RESULT 2
AAB81987
ID AAB81987 standard; protein; 582 AA.
XX
AC AAB81987;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 53.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Claim 41; Page 168-172; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 582 AA;

Query Match 98.5%; Score 3026; DB 4; Length 582;
Best Local Similarity 98.3%; Pred. No. 8.7e-147;
Matches 572; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

```
Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || |||||||||:|||||:|||||||||||||||||| | | ||||||||||||||||||
Db          1 EVQLVESGGDFVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAYISSGGSGTYY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSSA 120
              |||||||||||||:|||||||||||||:||||:|||||||||||||||||| ||||||
Db         61 SDSVKGRFTISRDNSKNTLYLQMRSLRAEDSAVYFCTRVKLGTYYFDSWGQGTLLTVSSA 120

Qy        121 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180

Qy        181 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 240

Qy        241 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300

Qy        301 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360

Qy        361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 420

Qy        421 QGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMILNGINNY 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 QGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMILNGINNY 480

Qy        481 KNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINV 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 KNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINV 540

Qy        541 IVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 582
              |||||||||||||||||||||||||||||||||||||||||||
Db        541 IVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 582
```

RESULT 3
AAB83156
ID AAB83156 standard; protein; 583 AA.
XX
AC AAB83156;
XX
DT 02-JUL-2001 (first entry)
XX
DE Ganglioside GM2 antibody-related protein #1.
XX
KW Ganglioside; GM2; antibody; cytostatic; cytotoxic; cancer.
XX
OS Unidentified.
XX

PN WO200123431-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006775.
XX
PR 30-SEP-1999; 99JP-00278292.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Nakamura K, Niwa R;
XX
DR WPI; 2001-266142/27.
XX
PT Monoclonal antibodies against ganglioside GM2 combined with drugs,
PT radioisotopes or proteins for treatment and diagnosis of cancer.
XX
PS Claim 43; Page 61-65; 80pp; Japanese.
XX
CC The present invention relates to derivatives of an antibody against
CC ganglioside GM2. The antibody may be a monoclonal antibody or its
CC fragments. The antibody is combined with a radioactive isotope, protein
CC or small drug in the treatment and diagnosis of cancer
XX
SQ Sequence 583 AA;

Query Match 89.9%; Score 2759.5; DB 4; Length 583;
Best Local Similarity 89.4%; Pred. No. 3.6e-133;
Matches 523; Conservative 21; Mismatches 36; Indels 5; Gaps 2;

```
Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||:|| :  ||| |:|||| |||: |: | | ||:|:| : |||: ||     || |
Db          1 EVQLVQSGAEVKKPGASVKVSCKASGYTFTDYNMDWVKQSPGQGLEWMGYIYPNNGGTGY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYY---FDSWGQGTTLTV 117
              :   | : ||: | : :| |::: ||||||:|:|:|     | ||   |  ||||| :||
Db         61 NQKFKSKVTITVDTSTSTAYMELHSLRSEDTAVYYC--ATYGHYYGYMFAYWGQGTLVTV 118

Qy        118 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        119 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 178

Qy        178 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        179 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 238

Qy        238 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 298

Qy        298 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        299 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 358

Qy        358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 418

Qy        418 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMILNGI 477
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        419 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMILNGI 478

Qy        478 NNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISN 537
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        479 NNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISN 538

Qy        538 INVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 582
              |||||||||||||||||||||||||||||||||||||||||||||
Db        539 INVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 583
```

RESULT 4
AAE33444

ID AAE33444 standard; protein; 579 AA.
XX
AC AAE33444;
XX
DT 02-APR-2003 (first entry)
XX
DE KS antibody heavy chain-interleukin 2 (IL-2) fusion protein.
XX
KW Immunoglobulin; diagnosis; epithelial cell adhesion molecule; EpCAM;
KW cancer; gene therapy; interleukin-2; IL2; fusion protein.
XX
OS Unidentified.
XX
PN WO200290566-A2.
XX
PD 14-NOV-2002.
XX
PF 03-MAY-2002; 2002WO-US013844.
XX
PR 03-MAY-2001; 2001US-0288564P.
XX
PA (LEXI-) LEXIGEN PHARM CORP.
XX
PI Gillies SD, Lo K, Qian X;
XX
DR WPI; 2003-111985/10.
DR N-PSDB; AAD51139.
XX
PT New recombinant anti-EpCAM antibody having an amino acid sequence
PT defining an immunoglobulin light or heavy chain framework region, useful
PT for the diagnosis, prognosis and treatment of cancer.
XX
PS Disclosure; Page 80-82; 82pp; English.
XX
CC The present invention relates to novel recombinant anti-EpCAM (human
CC epithelial cell adhesion molecule) antibodies comprising an amino acid
CC sequence defining an immunoglobulin light or heavy chain framework
CC region. Sequences of the present invention are useful for the diagnosis,
CC prognosis and treatment of cancer. They are also used in gene therapy.
CC The present sequence is KS antibody heavy chain-interleukin 2 (IL-2)
CC fusion protein. This sequence is used to illustrate the method of the
CC invention
XX
SQ Sequence 579 AA;

Query Match 89.4%; Score 2744.5; DB 6; Length 579;
Best Local Similarity 88.5%; Pred. No. 2.1e-132;
Matches 516; Conservative 31; Mismatches 31; Indels 5; Gaps 2;

```
Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              :: ||:|| :  ||| ::|:|| |||: |::| |:||:||| | |:|: :|::      |
Db          1 QIQLVQSGAEVKKPGETVKISCKASGYTFTNYGMNWVKQTPGKGLKWMGWINTYTGEPTY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTR-VKLGTYYFDSWGQGTTLTVSS 119
              :|  ||||  | : : :| :||: :|||||:| ||| | :  | |    |||||::||||
Db         61 ADDFKGRFAFSLETSTSTAFLQINNLRSEDTATYFCVRFISKGDY----WGQGTSVTVSS 116

Qy        120 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        117 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 176

Qy        180 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 239
              |||||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||
Db        177 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGG 236

Qy        240 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        237 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 296

Qy        300 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db        297 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE 356
```

```
Qy        360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 419
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        357 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 416

Qy        420 QQGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMILNGINN 479
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        417 QQGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMILNGINN 476

Qy        480 YKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNIN 539
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        477 YKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNIN 536

Qy        540 VIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 582
              |||||||||||||||||||||||||||||||||||||||||||
Db        537 VIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 579
```

RESULT 5
AAO30910
ID AAO30910 standard; protein; 579 AA.
XX
AC AAO30910;
XX
DT 22-SEP-2003 (first entry)
XX
DE dI-KS-ala-IL2 (D20T) variant protein.
XX
KW Cytokine; interleukin-2; IL-2; cancer; viral infection; immune disorder;
KW gene therapy; immunoglobulin; Ig; fusion protein; human.
XX
OS Homo sapiens.
OS Unidentified.
OS Chimeric.
XX
PN WO2003048334-A2.
XX
PD 12-JUN-2003.
XX
PF 04-DEC-2002; 2002WO-US038780.
XX
PR 04-DEC-2001; 2001US-0337113P.
PR 12-APR-2002; 2002US-0371966P.
XX
PA (EMDL-) EMD LEXIGEN RES CENT CORP.
XX
PI Gillies SD;
XX
DR WPI; 2003-513757/48.
XX
PT New fusion protein comprising a non-IL-2 moiety fused to a mutant IL-2
PT moiety, useful for preparing a composition for treating cancer, viral
PT infections or immune disorders.
XX
PS Example 10; Page 60-63; 71pp; English.
XX
CC The invention relates to cytokine fusion proteins with increased
CC therapeutic index and methods for increasing the therapeutic index of
CC such fusion proteins. The fusion protein comprises a non-interleukin-2
CC (IL-2) moiety fused to a mutant IL-2 moiety. It is useful for preparing a
CC composition for treating cancer, viral infections or immune disorders.
CC The fusion protein is also used in gene therapy. The present sequence is
CC dI-KS-ala-IL2 (D20T) variant protein comprising dI-KS heavy chain fused
CC to human IL-2 (D20T) variant protein. This sequence is used to illustrate
CC the method of the invention
XX
SQ Sequence 579 AA;

Query Match 89.2%; Score 2738.5; DB 6; Length 579;
Best Local Similarity 88.3%; Pred. No. 4.2e-132;
Matches 515; Conservative 30; Mismatches 33; Indels 5; Gaps 2;

```
Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              :: ||:|| :  ||| |:|:|| |||: |::| |:|||| | | |:|: :|::      |
Db          1 QIQLVQSGPELKKPGSSVKISCKASGYTFTNYGMNWVRQAPGKGLKWMGWINTYTGEPTY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTR-VKLGTYYFDSWGQGTTLTVSS 119
              :|  ||||||: : : :|||||: :|||||:| ||| | :  | |    ||||||:||||
Db         61 ADDFKGRFTITAETSTSTLYLQLNNLRSEDTATYFCVRFISKGDY----WGQGTTVTVSS 116

Qy        120 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        117 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 176

Qy        180 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 239
              |||||||||||||||||||||||||||||||||:|||||||||||||||||||||||||
Db        177 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGG 236

Qy        240 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        237 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 296

Qy        300 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db        297 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE 356

Qy        360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 419
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        357 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 416

Qy        420 QQGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMILNGINN 479
              |||||||||||||||||||| : :|| |||||||||||||||||| ||||||||||
Db        417 QQGNVFSCSVMHEALHNHYTQKSATATPGAAPTSSSTKKTQLQLEHLLLTLQMILNGINN 476

Qy        480 YKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNIN 539
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        477 YKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNIN 536

Qy        540 VIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 582
              |||||||||||||||||||||||||||||||||||||||||||
Db        537 VIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 579
```

RESULT 6
AAB81972
ID AAB81972 standard; protein; 581 AA.
XX
AC AAB81972;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD2 specific antibody related protein SEQ ID NO: 31.
XX
KW Ganglioside; GD2; complementation determining region; CDR; antibody;
KW mouse; cancer.
XX
OS Synthetic.
XX
PN WO200123573-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006773.
XX
PR 30-SEP-1999; 99JP-00278290.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266163/27.
XX
PT Human type complementation-determining domain transplanted antibody and
PT derivatives against ganglioside GD2, useful in diagnosis and therapy of
PT e.g. tumors, has low antigenicity, little side effects but potent
PT activity in cancer.
XX

PS Example 3; Page 111-114; 123pp; Japanese.
XX
CC The present invention describes an antibody, which can react specifically
CC with ganglioside GD2, and is transplanted with a human type
CC complementation-determining domain (CDR), or its fragments. The antibody
CC and its derivatives are useful in diagnosis and therapy of tumours,
CC particularly cancer diagnosis. The present sequence is a protein used in
CC the exemplification of the invention
XX
SQ Sequence 581 AA;

Query Match 88.9%; Score 2731.5; DB 4; Length 581;
Best Local Similarity 89.0%; Pred. No. 9.7e-132;
Matches 518; Conservative 24; Mismatches 39; Indels 1; Gaps 1;

```
Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              :| | |||   |||  :| ::|  |||: : | : |||| | | |||:  | :||| | |
Db          1 QVQLQESGPGLVKPSQTLSITCTVSGFSLASYNIHWVRQPPGKGLEWLGVIWAGGS-TNY 59

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSSA 120
              : ::  | |||:||:|| ::|:|  || : |:|:|:|  :      :|  ||||| :|||||
Db         60 NSALMSRLTISKDNSKNQVFLKMSSLTAADTAVYYCAKRSDDYSWFAYWGQGTLVTVSSA 119

Qy        121 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 179

Qy        181 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 239

Qy        241 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 299

Qy        301 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 359

Qy        361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 419

Qy        421 QGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMILNGINNY 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 QGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMILNGINNY 479

Qy        481 KNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINV 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 KNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINV 539

Qy        541 IVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 582
              |||||||||||||||||||||||||||||||||||||||||||
Db        540 IVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 581
```

RESULT 7
ADP42961
ID ADP42961 standard; protein; 575 AA.
XX
AC ADP42961;
XX
DT 23-SEP-2004 (first entry)
XX
DE Humanised immunoglobulin heavy chain-IL-2 fusion protein SEQ ID NO:6.
XX
KW immunoglobulin; variable region; antibody; GD2; cytostatic; gene therapy;
KW cancer; cell surface glycosphingolipid; IL-2.
XX
OS Synthetic.
XX
PN WO2004055056-A1.
XX
PD 01-JUL-2004.
XX
PF 16-DEC-2003; 2003WO-EP014295.
XX
PR 17-DEC-2002; 2002US-0433945P.
XX
PA (MERE) MERCK PATENT GMBH.
XX
PI Gillies SD, Lo K;
XX
DR WPI; 2004-488049/46.
DR N-PSDB; ADP42959.
XX
PT New modified m14.18 antibodies with reduced immunogenicity and that
PT specifically bind the human cell surface glycosphingolipid GD2, useful
PT for treating cancer.
XX
PS Disclosure; SEQ ID NO 6; 51pp; English.
XX
CC The invention relates to a novel antibody variable region, where the
CC antibody variable region specifically binds to human cell surface
CC glycosphingolipid GD2. An antibody variable region of the invention has
CC cytostatic activity, and may have a use in gene therapy. The antibody may
CC be used for treating cancer. The nucleic acid or cell is useful for
CC manufacturing a medicament that may be used for treating diseases such as
CC cancer. The present sequence represents an immunoglobulin heavy chain-IL-
CC 2 fusion protein.
XX
SQ Sequence 575 AA;

Query Match 88.4%; Score 2715.5; DB 8; Length 575;
Best Local Similarity 88.8%; Pred. No. 6.3e-131;
Matches 517; Conservative 24; Mismatches 34; Indels 7; Gaps 3;

```
Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||:|| :  ||| |:|:|| ||| :|: | |:||||   | |||:  |`   || |
Db          1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSSA 120
              :   ||| |:: | : :| |: ::||||||:|:|:|     |  |   |||||::|||||
Db         61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDTAVYYCVS---GMEY---WGQGTSVTVSSA 114

Qy        121 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 174

Qy        181 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 240
              ||||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||
Db        175 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGP 234

Qy        241 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 294

Qy        301 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|:||
Db        295 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM 354

Qy        361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 414

Qy        421 QGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMILNGINNY 480
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db        415 QGNVFSCSVMHEALHNHYTQKSLSLSPG-APTSSSTKKTQLQLEHLLLDLQMILNGINNY 473

Qy        481 KNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINV 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 KNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINV 533

Qy        541 IVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 582
              |||||||||||||||||||||||||||||||||||||||||||
Db        534 IVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 575
```

```
RESULT 8
AAO30915
ID   AAO30915 standard; protein; 580 AA.
XX
AC   AAO30915;
XX
DT   22-SEP-2003  (first entry)
XX
DE   dI-NHS76 (gamma4h) (FN>AQ)-ala-IL2 (D20T) variant protein.
XX
KW   Cytokine; interleukin-2; IL-2; cancer; viral infection; immune disorder;
KW   gene therapy; immunoglobulin; Ig; fusion protein; human; variant.
XX
OS   Homo sapiens.
OS   Unidentified.
OS   Chimeric.
XX
PN   WO2003048334-A2.
XX
PD   12-JUN-2003.
XX
PF   04-DEC-2002; 2002WO-US038780.
XX
PR   04-DEC-2001; 2001US-0337113P.
PR   12-APR-2002; 2002US-0371966P.
XX
PA   (EMDL-) EMD LEXIGEN RES CENT CORP.
XX
PI   Gillies SD;
XX
DR   WPI; 2003-513757/48.
XX
PT   New fusion protein comprising a non-IL-2 moiety fused to a mutant IL-2
PT   moiety, useful for preparing a composition for treating cancer, viral
PT   infections or immune disorders.
XX
PS   Example 10; Page 68-71; 71pp; English.
XX
CC   The invention relates to cytokine fusion proteins with increased
CC   therapeutic index and methods for increasing the therapeutic index of
CC   such fusion proteins. The fusion protein comprises a non-interleukin-2
CC   (IL-2) moiety fused to a mutant IL-2 moiety. It is useful for preparing a
CC   composition for treating cancer, viral infections or immune disorders.
CC   The fusion protein is also used in gene therapy. The present sequence is
CC   dI-NHS76 (gamma4h) (FN>AQ)-ala-IL2 (D20T) variant protein comprising dI-
CC   KS heavy chain fused to human IL-2 (D20T) variant protein. This sequence
CC   is used to illustrate the method of the invention
XX
SQ   Sequence 580 AA;

  Query Match             84.4%;  Score 2592;  DB 6;  Length 580;
  Best Local Similarity   84.7%;  Pred. No. 1.3e-124;
  Matches  494;  Conservative   31;  Mismatches   54;  Indels    4;  Gaps    3;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSH-YAMSWVRQTPAKRLEWVAYISSGGSGTY 59
              :| | |||   |||  :| ::|| ||:: |  |   |:|| | | |||:  |   || ||
Db          1 QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYWGWIRQPPGKGLEWIGSIYHSGS-TY 59

Qy         60 YSDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
              |: |:| | ||| | :||   |:: |: : |:|:|:| | |     || ||||| :||||
Db         60 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGKWSK--FDYWGQGTLVTVSS 117

Qy        120 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
              |||||||||||||  |:|||  ||||||||||||||||||||||||||||||||||||||
Db        118 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 177

Qy        180 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 239
              ||||||||||||||||:|| |||:||||||||||:||||||||||||||||||| |||
Db        178 GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEFLGG 237

Qy        240 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299
              |||||||||||||||||||||||||||||| |||||:||||||||||||||||||||||
Db        238 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQAQ 297

Qy        300 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359
              |||||||||||||||||||||||||||||| ||: |||||||||||||||||||||::|
Db        298 STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEE 357

Qy        360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 419
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 417

Qy        420 QQGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMILNGINN 479
              ||||:|||||||||||||||| : :|| |||||||||||||||| ||||||||||
Db        418 QQGNIFSCSVMHEALHNHYTQKSATATPGAAPTSSSTKKTQLQLEHLLLTLQMILNGINN 477

Qy        480 YKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNIN 539
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 YKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNIN 537

Qy        540 VIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 582
              |||||||||||||||||||||||||||||||||||||||||||
Db        538 VIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 580


RESULT 9
AAO30913
ID   AAO30913 standard; protein; 580 AA.
XX
AC   AAO30913;
XX
DT   22-SEP-2003  (first entry)
XX
DE   dI-NHS76 (gamma2h) (FN>AQ)-ala-IL2 (D20T) variant protein.
XX
KW   Cytokine; interleukin-2; IL-2; cancer; viral infection; immune disorder;
KW   gene therapy; immunoglobulin; Ig; fusion protein; human; variant.
XX
OS   Homo sapiens.
OS   Unidentified.
OS   Chimeric.
XX
PN   WO2003048334-A2.
XX
PD   12-JUN-2003.
XX
PF   04-DEC-2002; 2002WO-US038780.
XX
PR   04-DEC-2001; 2001US-0337113P.
PR   12-APR-2002; 2002US-0371966P.
XX
PA   (EMDL-) EMD LEXIGEN RES CENT CORP.
XX
PI   Gillies SD;
XX
DR   WPI; 2003-513757/48.
XX
PT   New fusion protein comprising a non-IL-2 moiety fused to a mutant IL-2
PT   moiety, useful for preparing a composition for treating cancer, viral
PT   infections or immune disorders.
XX
PS   Claim 37; Page 64-67; 71pp; English.
XX
CC   The invention relates to cytokine fusion proteins with increased
CC   therapeutic index and methods for increasing the therapeutic index of
CC   such fusion proteins. The fusion protein comprises a non-interleukin-2
CC   (IL-2) moiety fused to a mutant IL-2 moiety. It is useful for preparing a
CC   composition for treating cancer, viral infections or immune disorders.
CC   The fusion protein is also used in gene therapy. The present sequence is
CC   dI-NHS76 (gamma2h) (FN>AQ)-ala-IL2 (D20T) variant protein comprising dI-
CC   KS heavy chain fused to human IL-2 (D20T) variant protein. This sequence
CC   is used to illustrate the method of the invention
XX
SQ   Sequence 580 AA;
```

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  Query Match             83.4%;  Score 2560;  DB 6;  Length 580;
  Best Local Similarity   84.1%;  Pred. No. 5.6e-123;
  Matches  491;  Conservative   31;  Mismatches   56;  Indels    6;  Gaps    5;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSH-YAMSWVRQTPAKRLEWVAYISSGGSGTY 59
              :| | |||   |||  :| ::|| ||:: |  |   |:|| | | |||:  |   || ||
Db          1 QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYWGWIRQPPGKGLEWIGSIYHSGS-TY 59

Qy         60 YSDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSS 119
              |: |:| | ||| | :||   |:: |: : |:|:|:| | |     || ||||| :||||
Db         60 YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGKWSK--FDYWGQGTLVTVSS 117

Qy        120 -ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 178
               |||||||||||||| |:||| |||||||||||||||||||||||||||||||||||||||
Db        118 GASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 177

Qy        179 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 238
              |||||||||||||||: ||||| |||:|||||||||| |||||||||||||||||||  :
Db        178 SGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVEPKSCDKTHTCPPCPAPP-VA 236

Qy        239 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 298
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Db        237 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQA 296

Qy        299 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 358
              ||:|||||||:|||||||||||||||| |||||||||| ||||||||||||||||||:
Db        297 QSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSRE 356

Qy        359 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 418
              |:|||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db        357 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSR 416

Qy        419 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMILNGIN 478
              |||||||||||||||||||| : :|| |||||||||||||||| |||||||||
Db        417 WQQGNVFSCSVMHEALHNHYTQKSATATPGAAPTSSSTKKTQLQLEHLLLTLQMILNGIN 476

Qy        479 NYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNI 538
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        477 NYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNI 536

Qy        539 NVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 582
              |||||||||||||||||||||||||||||||||||||||||||
Db        537 NVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 580


RESULT 10
AAO18400
ID   AAO18400 standard; protein; 449 AA.
XX
AC   AAO18400;
XX
DT   11-OCT-2002  (first entry)
XX
DE   Mature humanised murine CBE11 heavy chain variable domain.
XX
KW   Mouse; humanised antibody; lymphotoxin beta receptor; antibody; cancer;
KW   neoplasia; LT-beta-R; light chain; heavy chain; variable region.
XX
OS   Mus sp.
OS   Synthetic.
XX
PN   WO200230986-A2.
XX
PD   18-APR-2002.
XX
PF   12-OCT-2001; 2001WO-US032140.
XX
PR   13-OCT-2000; 2000US-0240285P.
PR   13-MAR-2001; 2001US-0275289P.
PR   21-JUN-2001; 2001US-0299987P.
XX
PA   (BIOJ ) BIOGEN INC.
XX
PI   Garber E,  Lyne P,  Saldanha JW;
XX
DR   WPI; 2002-583337/62.
XX
PT   New humanized anti-lymphotoxin-beta receptor antibody, useful for
PT   treating or reducing the advancement, severity or effects of neoplasia,
PT   particularly solid tumors (i.e. carcinomas) including colorectal cancer
PT   and breast cancer.
XX
PS   Example 5; Page 25-26; 41pp; English.
XX
CC   The present invention relates to humanised anti-lymphotoxin beta receptor
CC   (LT-beta-R) antibodies. These are derived from the murine LT-beta-R
CC   binding antibody CBE11 and can be used to treat neoplasia in humans. The
CC   present sequence is a humanised murine CBE11 heavy chain variable region
XX
SQ   Sequence 449 AA;

  Query Match             72.2%;  Score 2218.5;  DB 5;  Length 449;
  Best Local Similarity   93.1%;  Pred. No. 1.2e-105;
  Matches  418;  Conservative    9;  Mismatches   21;  Indels    1;  Gaps    1;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||  |||||||::|||||| || | | | || | | ||||| || ||| |||
Db          1 EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMYWFRQAPGKGLEWVATISDGGSYTYY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGT-YYFDSWGQGTTLTVSS 119
              |||||||||||||||:|||| ||||:||:|:|:| | : |  |||| ||||||:||||
Db         61 PDSVKGRFTISRDNAKNSLYLQMSSLRAEDTAVYYCAREENGNFYYFDYWGQGTTVTVSS 120

Qy        120 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 180

Qy        180 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 240

Qy        240 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 300

Qy        300 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 360

Qy        360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 419
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 420

Qy        420 QQGNVFSCSVMHEALHNHYTQKSLSLSPG 448
              |||||||||||||||||||||||||||||
Db        421 QQGNVFSCSVMHEALHNHYTQKSLSLSPG 449


RESULT 11
ADN97491
ID   ADN97491 standard; protein; 713 AA.
XX
AC   ADN97491;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Artificial protein construction protein #4.
XX
KW   artificial proprotein; propeptide; protein engineering; antibody.
XX
OS   Unidentified.
XX
PN   WO2004031362-A2.
XX
PD   15-APR-2004.
```

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XX
PF   03-OCT-2003; 2003WO-US031420.
XX
PR   03-OCT-2002; 2002US-0415940P.
XX
PA   (LARG-) LARGE SCALE BIOLOGY CORP.
XX
PI   Reini SJ,  Edwards P;
XX
DR   WPI; 2004-330170/30.
DR   N-PSDB; ADN97490.
XX
PT   New artificial proprotein comprises three peptide sequences, useful for
PT   artificial multimeric protein engineering in eukaryotes.
XX
PS   Example 15; SEQ ID NO 64; 244pp; English.
XX
CC   The invention relates to an artificial proprotein comprising three
CC   peptide sequences: a first peptide sequence of interest, a propeptide
CC   sequence attached to the C-terminus of the first peptide sequence of
CC   interest, and a second peptide of interest attached to the C-terminus of
CC   the propeptide sequence. The artificial proprotein and polynucleotides
CC   are useful for artificial multimeric protein engineering, e.g. antibodies
CC   and antibody fragments in eukaryotes. This sequence corresponds to a
CC   protein used in the generation of the protein of the invention.
XX
SQ   Sequence 713 AA;

  Query Match             72.2%;  Score 2216;  DB 8;  Length 713;
  Best Local Similarity   91.7%;  Pred. No. 2.6e-105;
  Matches  419;  Conservative   10;  Mismatches   20;  Indels    8;  Gaps    2;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||| |||||||:|||||| |||| |||||||| ||||||| | | |: |:|
Db        257 EVDLVESGGDLVKPGGSLKLSCAASGFTFSHYGMSWVRQTPDKRLEWVATIGSRGTYTHY 316

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKL-----GTYYF---DSWGQG 112
              |||||||||||| || ||||| ||:|||:|||:| |         |||:   | ||||
Db        317 PDSVKGRFTISRDNDKNALYLQMNSLKSEDTAMYYCARRSEFYYYGNTYYYSAMDYWGQG 376

Qy        113 TTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 172
               ::|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 ASVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 436

Qy        173 PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCP 232
              ||||||||||||||||||||||||||||||||||||||:|||||||||||||||||
Db        437 PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP 496

Qy        233 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        497 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 556

Qy        293 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        557 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT 616

Qy        353 LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL 412
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        617 LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL 676

Qy        413 TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||||||||||||||||||||||
Db        677 TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 713


RESULT 12
ADN97489
ID   ADN97489 standard; protein; 715 AA.
XX
AC   ADN97489;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Artificial protein construction protein #3.
XX
KW   artificial proprotein; propeptide; protein engineering; antibody.
XX
OS   Unidentified.
XX
PN   WO2004031362-A2.
XX
PD   15-APR-2004.
XX
PF   03-OCT-2003; 2003WO-US031420.
XX
PR   03-OCT-2002; 2002US-0415940P.
XX
PA   (LARG-) LARGE SCALE BIOLOGY CORP.
XX
PI   Reini SJ,  Edwards P;
XX
DR   WPI; 2004-330170/30.
DR   N-PSDB; ADN97488.
XX
PT   New artificial proprotein comprises three peptide sequences, useful for
PT   artificial multimeric protein engineering in eukaryotes.
XX
PS   Example 15; SEQ ID NO 62; 244pp; English.
XX
CC   The invention relates to an artificial proprotein comprising three
CC   peptide sequences: a first peptide sequence of interest, a propeptide
CC   sequence attached to the C-terminus of the first peptide sequence of
CC   interest, and a second peptide of interest attached to the C-terminus of
CC   the propeptide sequence. The artificial proprotein and polynucleotides
CC   are useful for artificial multimeric protein engineering, e.g. antibodies
CC   and antibody fragments in eukaryotes. This sequence corresponds to a
CC   protein used in the generation of the protein of the invention.
XX
SQ   Sequence 715 AA;

  Query Match             72.2%;  Score 2216;  DB 8;  Length 715;
  Best Local Similarity   91.7%;  Pred. No. 2.6e-105;
  Matches  419;  Conservative   10;  Mismatches   20;  Indels    8;  Gaps    2;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||| |||||||:|||||| |||| |||||||| ||||||| | | |: |:|
Db        259 EVDLVESGGDLVKPGGSLKLSCAASGFTFSHYGMSWVRQTPDKRLEWVATIGSRGTYTHY 318

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKL-----GTYYF---DSWGQG 112
              |||||||||||| || ||||| ||:|||:|||:| |         |||:   | ||||
Db        319 PDSVKGRFTISRDNDKNALYLQMNSLKSEDTAMYYCARRSEFYYYGNTYYYSAMDYWGQG 378

Qy        113 TTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 172
               ::|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 ASVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 438

Qy        173 PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCP 232
              ||||||||||||||||||||||||||||||||||||||:|||||||||||||||||
Db        439 PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP 498

Qy        233 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 558

Qy        293 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT 618

Qy        353 LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL 412
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL 678

Qy        413 TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||||||||||||||||||||||
Db        679 TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 715
```

```
RESULT 13
ADM47075
ID   ADM47075 standard; protein; 475 AA.
XX
AC   ADM47075;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Mouse anti-human G-CSF antibody heavy chain protein.
XX
KW   methylotroph yeast; mammalian sugar chain; OCH1; alpha-1;
KW   6-mannosyl transferase; alpha-1; 2-mannosidase;
KW   orotidin-5'-phosphate decarboxylase; URA3;
KW   phosphoribosyl-amino-imidazole succinocarboxamide synthase; ADE1;
KW   imidazole-glycerol-phosphate dehydratase; HIS3;
KW   3-isopropyl malate dehydrogenase; LEU2; proteinase A; proteinase B; PRB1;
KW   PEP4; YPS1; KTR1; MNN9; AOX; GAPDH; mannosyl transferase;
KW   glyceraldehyde 3-phosphate dehydrogenase; mannose glycoprotein.
XX
OS   Mus sp.
XX
PN   WO2003091431-A1.
XX
PD   06-NOV-2003.
XX
PF   28-APR-2003; 2003WO-JP005464.
XX
PR   26-APR-2002; 2002JP-00127677.
XX
PA   (KIRI ) KIRIN BEER KK.
PA   (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX
PI   Kobayashi K,  Kitagawa Y,  Komeda T,  Kawashima N,  Jigami Y;
PI   Chiba Y;
XX
DR   WPI; 2003-854401/79.
XX
PT   Producing methylotroph yeast that expresses mammalian sugar chains by
PT   disrupting the OCH1 gene and inserting an alpha-1,2-mannosidase gene.
XX
PS   Example 28; SEQ ID NO 94; 247pp; Japanese.
XX
CC   The invention relates to the production of a methylotroph yeast that
CC   produces mammalian sugar chains, comprising disrupting the OCH1 gene in
CC   the yeast that encodes for alpha-1,6-mannosyl transferase and inserting
CC   and expressing the alpha-1,2-mannosidase gene. The specification also
CC   includes DNA sequences encoding: (a) orotidin-5'-phosphate decarboxylase
CC   (URA3); (b) phosphoribosyl-amino-imidazole succinocarboxamide synthase
CC   (ADE1); (c) imidazole-glycerol-phosphate dehydratase (HIS3); (d) 3-
CC   isopropyl malate dehydrogenase (LEU2); (e) alpha-1,6-mannosyl transferase
CC   (OCH1); (f) proteinase A (PEP4); (g) proteinase B (PRB1); and (h)
CC   aspartic protease (YPS1), mannosyl transferase (KTR1 or MNN9), alcohol
CC   oxidase (AOX) and glyceraldehyde 3-phosphate dehydrogenase (GAPDH) gene
CC   sequences. The yeast is used for the production of human and mammalian
CC   high mannose glycoproteins with high yield and purity. The method is also
CC   useful for producing hybrid or complex sugar chains containing mammalian
CC   type chains. This sequence represents a mouse anti-human G-CSF antibody
CC   heavy chain used in the invention.
XX
SQ   Sequence 475 AA;

  Query Match             71.9%;  Score 2209.5;  DB 7;  Length 475;
  Best Local Similarity   91.2%;  Pred. No. 3.7e-105;
  Matches  416;  Conservative   15;  Mismatches   18;  Indels    7;  Gaps    2;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||  |||||||::|||||| || |:|:|||| | | ||||: ||| |  ||
Db         20 EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYY 79

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKL----GTYYF---DSWGQGT 113
              :|||||||||||||||:|||| |||:||:|:|:| | ::    | ||:   | |||||
Db         80 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDRIIMVRGVYYYYGMDVWGQGT 139

Qy        114 TLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 173
              |:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 TVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 199

Qy        174 AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA 259

Qy        234 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 319

Qy        294 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 379

Qy        354 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 413
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 439

Qy        414 VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              ||||||||||||||||||||||||||||||||||||
Db        440 VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 475


RESULT 14
AAR47453
ID   AAR47453 standard; protein; 477 AA.
XX
AC   AAR47453;
XX
DT   25-MAR-2003  (revised)
DT   24-JUN-1994  (first entry)
XX
DE   chiT84.12 H3 heavy chain.
XX
KW   Chimeric; carcinoembryonic antigen; CCA; murine; mouse; constant; region;
KW   transform; myeloma cell; light chain; tumour.
XX
OS   Synthetic.
XX
PN   WO9325237-A1.
XX
PD   23-DEC-1993.
XX
PF   15-JUN-1993;   93WO-US005709.
XX
PR   15-JUN-1992;   92US-00904074.
XX
PA   (YANG/) YANG Y.
PA   (CITY ) CITY OF HOPE.
XX
PI   Shively JE,  Fischer R,  Wu A,  Paxton R,  Yang YH;
XX
DR   WPI; 1994-007204/01.
DR   N-PSDB; AAQ54655.
XX
PT   New chimeric T 84.12 antibody active against carcinoembryonic antigen -
PT   has murine variable and human constant regions, also DNA encoding it and
PT   transformed myeloma cells.
XX
PS   Claim 1; Page 22-23; 27pp; English.
XX
CC   The sequences (AAQ54651-52) show the light and heavy chain cDNAs of
CC   murine T84.12. The T84.12 antibody is directed against the tumour marker
CC   carcinoma embryonic antigen, and is useful for tumour imaging and
CC   immunotherapy. The amino acid sequence given in the specification has
CC   been incorrectly identified as a nucleic acid sequence, therefore
CC   unacceptable characters have been represented as an 'N'. The amino acid
CC   sequence given below has been derived from the cDNA, by the indexer.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
```

```
SQ   Sequence 477 AA;

  Query Match             71.8%;  Score 2205;  DB 2;  Length 477;
  Best Local Similarity   92.5%;  Pred. No. 6.3e-105;
  Matches  419;  Conservative    8;  Mismatches   18;  Indels    8;  Gaps    3;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || |||||| |||||||||:||||||| || |||||||||| ||||||| ||| |  |:|
Db         29 EVKLVESGGGFVKPGGSLKLSCAASGFTFSSYAMSWVRQTPEKRLEWVASISSDGI-TFY 87

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYY----FDSWGQGTTLT 116
               ||||||||:|||||:| ||||| |||||:|||:| |:    ||     |  |||||  |
Db         88 VDSVKGRFTVSRDNARNILYLQMSSLRSEDTAMYYCARI---DYYGGGGFGYWGQGTLAT 144

Qy        117 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 176
              ||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 VSAASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 204

Qy        177 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 264

Qy        237 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 296
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        265 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDASHEDPEVKFNWYVDGVEVHNAKTKPREE 324

Qy        297 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 384

Qy        357 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 416
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 444

Qy        417 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||||||||||||||||||
Db        445 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 477


RESULT 15
ADM72029
ID   ADM72029 standard; protein; 471 AA.
XX
AC   ADM72029;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Chimeric mouse-human antibody M19B11 heavy chain.
XX
KW   GPC3; glypican 3; anti-GPC3 antibody; cell disruption; anti-cancer;
KW   cytostatic; M19B11.
XX
OS   Mus sp.
OS   Homo sapiens.
OS   Chimeric.
XX
PN   WO2004022739-A1.
XX
PD   18-MAR-2004.
XX
PF   04-SEP-2003; 2003WO-JP011318.
XX
PR   04-SEP-2002; 2002WO-JP008999.
XX
PA   (CHUS ) CHUGAI SEIYAKU KK.
XX
PI   Aburatani H,  Midorikawa Y,  Nakano K,  Ohizumi I,  Ito Y,  Tokita S;
XX
DR   WPI; 2004-269573/25.
DR   N-PSDB; ADM72028.
XX
PT   Antibody against the N terminus of glypican 3(GPC3) causes cell
PT   disruption and is useful as an anticancer agent.
XX
PS   Example 4; SEQ ID NO 14; 122pp; Japanese.
XX
CC   The invention relates to an antibody against the N terminus of glypican 3
CC   (GPC3). The antiboduy can be used for causing cell disruption and can be
CC   uses as an anti-cancer agent. The present sequence represents a chimeric
CC   mouse-human antibody M19B11 heavy chain.
XX
SQ   Sequence 471 AA;

  Query Match             71.8%;  Score 2203.5;  DB 8;  Length 471;
  Best Local Similarity   92.3%;  Pred. No. 7.5e-105;
  Matches  418;  Conservative    9;  Mismatches   21;  Indels    5;  Gaps    2;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||| |||||:||:|||||  ||:|||||||||| ||||||| | | |  |||
Db         20 EVQLVESGGDLVKPGGTLKLSCAASGSTFSNYAMSWVRQTPEKRLEWVAAIDSNGGTTYY 79

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTY----YFDSWGQGTTLT 116
                |::| |||||||||||||||| ||||||:| | |||   | |    :|  ||||| :|
Db         80 PDTMKDRFTISRDNAKNTLYLQMNSLRSEDTAFYHCTRHN-GGYENYGWFAYWGQGTLVT 138

Qy        117 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 176
              ||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 VSAASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 198

Qy        177 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 258

Qy        237 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 318

Qy        297 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 378

Qy        357 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 416
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 438

Qy        417 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||||||||||||||||||
Db        439 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 471


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OM protein - protein search, using sw model

Run on: December 23, 2004, 18:46:39 ; Search time 38.4376 Seconds
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2153.5	70.1	459	1	US-08-157-101A-7	Sequence 7, Appli
2	2149.5	70.0	452	3	US-09-027-449-71	Sequence 71, Appl
3	2149.5	70.0	452	3	US-09-026-985-71	Sequence 71, Appl
4	2149.5	70.0	452	4	US-09-121-952A-71	Sequence 71, Appl
5	2149.5	70.0	452	4	US-09-234-340A-71	Sequence 71, Appl
6	2124	69.2	453	3	US-08-466-151-8	Sequence 8, Appli
7	2124	69.2	453	3	US-08-466-163B-8	Sequence 8, Appli
8	2124	69.2	453	4	US-09-802-096-8	Sequence 8, Appli
9	2124	69.2	453	4	US-09-802-077-8	Sequence 8, Appli
10	2122	69.1	451	2	US-08-887-352B-14	Sequence 14, Appl
11	2122	69.1	451	2	US-08-887-352B-16	Sequence 16, Appl
12	2122	69.1	451	3	US-08-466-151-65	Sequence 65, Appl
13	2122	69.1	451	3	US-09-109-207C-14	Sequence 14, Appl
14	2122	69.1	451	3	US-09-109-207C-16	Sequence 16, Appl
15	2122	69.1	451	3	US-09-296-005-14	Sequence 14, Appl
16	2122	69.1	451	3	US-09-296-005-16	Sequence 16, Appl
17	2122	69.1	451	4	US-09-920-171-14	Sequence 14, Appl
18	2122	69.1	451	4	US-09-920-171-16	Sequence 16, Appl
19	2122	69.1	451	4	US-09-716-028-14	Sequence 14, Appl
20	2122	69.1	451	4	US-09-716-028-16	Sequence 16, Appl
21	2122	69.1	451	4	US-10-113-996-14	Sequence 14, Appl
22	2122	69.1	451	4	US-10-113-996-16	Sequence 16, Appl
23	2118	69.0	451	2	US-08-887-352B-18	Sequence 18, Appl
24	2118	69.0	451	3	US-09-109-207C-18	Sequence 18, Appl
25	2118	69.0	451	3	US-09-282-505-2	Sequence 2, Appli
26	2118	69.0	451	3	US-09-054-255-2	Sequence 2, Appli
27	2118	69.0	451	3	US-09-296-005-18	Sequence 18, Appl
28	2118	69.0	451	4	US-09-282-846-2	Sequence 2, Appli
29	2118	69.0	451	4	US-09-680-145-2	Sequence 2, Appli
30	2118	69.0	451	4	US-09-920-171-18	Sequence 18, Appl
31	2118	69.0	451	4	US-09-716-028-18	Sequence 18, Appl
32	2118	69.0	451	4	US-09-483-588-2	Sequence 2, Appli
33	2118	69.0	451	4	US-10-113-996-18	Sequence 18, Appl
34	2115.5	68.9	449	3	US-09-679-397-2	Sequence 2, Appli
35	2115.5	68.9	449	4	US-09-680-148-2	Sequence 2, Appli
36	2115.5	68.9	449	4	US-09-304-465A-2	Sequence 2, Appli
37	2102	68.4	449	1	US-08-458-516-13	Sequence 13, Appl
38	2097	68.3	478	3	US-08-487-550-8	Sequence 8, Appli
39	2097	68.3	478	4	US-09-526-098-8	Sequence 8, Appli
40	2097	68.3	478	4	US-09-383-916-8	Sequence 8, Appli
41	2066	67.3	711	3	US-09-485-737B-90	Sequence 90, Appl
42	2063	67.2	468	3	US-09-485-737B-67	Sequence 67, Appl
43	2052.5	66.8	467	4	US-08-030-175-42	Sequence 42, Appl
44	2052	66.8	476	2	US-08-378-939-10	Sequence 10, Appl
45	2049.5	66.7	467	4	US-08-030-175-41	Sequence 41, Appl

ALIGNMENTS

RESULT 1
US-08-157-101A-7
; Sequence 7, Application US/08157101A
; Patent No. 5808032
; GENERAL INFORMATION:
; APPLICANT: KURIHARA, TATSUYA
; APPLICANT: MATSUKURA, SHIGEKAZU
; APPLICANT: TSURUOKA, NOBUO
; APPLICANT: ARIMA, KENJI
; APPLICANT: NISHIHARA, TATSURO
; TITLE OF INVENTION: ANTI-HBs ANTIBODY GENES AND EXPRESSION
; TITLE OF INVENTION: PLASMIDS THEREFOR
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/157,101A
; FILING DATE: 05-APR-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: TITUS, MARLANA K
; REGISTRATION NUMBER: 35843
; REFERENCE/DOCKET NUMBER: 9437/204199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3711
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUCH
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 459 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-157-101A-7

Query Match 70.1%; Score 2153.5; DB 1; Length 459;
Best Local Similarity 89.8%; Pred. No. 1.3e-159;
Matches 404; Conservative 20; Mismatches 25; Indels 1; Gaps 1;

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Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              :| ||||||  |:|| ||::||||||| ||  :| |||| | | ||||| |   |:  :|
Db         10 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSNSMHWVRQAPGKGLEWVAVILYDGNHKFY 69

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVK-LGTYYFDSWGQGTTLTVSS 119
              :|||||||||||||:||||||:::||::||: :|:| | :  | : |||||||| :||||
Db         70 ADSVKGRFTISRDNSKNTLYLEVKSLQTEDTGVYYCIRDQTYGVHRFDSWGQGTLVTVSS 129

Qy        120 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        130 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALASGVHTFPAVLQSS 189

Qy        180 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 249

Qy        240 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 309

Qy        300 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 369

Qy        360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 419
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 429

Qy        420 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
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Db        430 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 459
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RESULT 2
US-09-027-449-71
; Sequence 71, Application US/09027449
; Patent No. 6025158
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/027,449
; FILING DATE: 20-Feb-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/074,330
; FILING DATE: 22-Jan-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/038,664
; FILING DATE: 21-Feb-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R3-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-027-449-71

Query Match 70.0%; Score 2149.5; DB 3; Length 452;
Best Local Similarity 88.7%; Pred. No. 2.6e-159;
Matches 401; Conservative 19; Mismatches 29; Indels 3; Gaps 1;

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Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||:|||  |:|||||::||||||:|| : | |||| | | |||| ||       | |
Db          1 EVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMHWVRQAPGKGLEWVGYIDPSNGETTY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKL---GTYYFDSWGQGTTLTV 117
              :   |||||:||||:||| |||| |||:||:|:|:| |      | ::|| ||||| :||
Db         61 NQKFKGRFTLSRDNSKNTAYLQMNSLRAEDTAVYYCARGDYRYNGDWFFDVWGQGTLVTV 120

Qy        118 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 180

Qy        178 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 240

Qy        238 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 300

Qy        298 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 360

Qy        358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 417
              :|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 420

Qy        418 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              ||||||||||||||||||||||||||||||||
Db        421 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 452
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RESULT 3
US-09-026-985-71
; Sequence 71, Application US/09026985
; Patent No. 6133426
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/026,985
; FILING DATE: 20-Feb-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.

```
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  P1085R3-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-5530
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  71:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  452 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-09-026-985-71

  Query Match            70.0%;  Score 2149.5;  DB 3;  Length 452;
  Best Local Similarity   88.7%;  Pred. No. 2.6e-159;
  Matches  401;  Conservative   19;  Mismatches   29;  Indels    3;  Gaps    1;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||:|||  |:|||||::|||||::|| : | |||| | | |||| ||      | |
Db          1 EVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMHWVRQAPGKGLEWVGYIDPSNGETTY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKL---GTYYFDSWGQGTTLTV 117
              :  |||||:||||:||| |||| |||:||:|:|:| |      | ::|| ||||| :||
Db         61 NQKFKGRFTLSRDNSKNTAYLQMNSLRAEDTAVYYCARGDYRYNGDWFFDVWGQGTLVTV 120

Qy        118 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 180

Qy        178 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 240

Qy        238 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 300

Qy        298 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 360

Qy        358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 417
              :|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 420

Qy        418 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              ||||||||||||||||||||||||||||||||
Db        421 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 452


RESULT 4
US-09-121-952A-71
; Sequence 71, Application US/09121952A
; Patent No. 6458355
;  GENERAL INFORMATION:
;    APPLICANT:  Genentech, Inc., Hsei, Vanessa
;    APPLICANT:  Koumenis, Iphigenia
;    APPLICANT:  Leong, Steven R.
;    APPLICANT:  Presta, Leonard G.
;    APPLICANT:  Shahrokh, Zahra
;    APPLICANT:  Zapata, Gerardo A.
;    TITLE OF INVENTION:  METHODS OF TREATING INFLAMMATORY DISEASES
;    TITLE OF INVENTION:  WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
;    NUMBER OF SEQUENCES:  72
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/121,952A
;      FILING DATE:  24-Jul-1998
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/074330
;      FILING DATE:  22-JAN-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/075467
;      FILING DATE:  20-FEB-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  P1085R4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-5530
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  71:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  452 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-09-121-952A-71

  Query Match            70.0%;  Score 2149.5;  DB 4;  Length 452;
  Best Local Similarity   88.7%;  Pred. No. 2.6e-159;
  Matches  401;  Conservative   19;  Mismatches   29;  Indels    3;  Gaps    1;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||:|||  |:|||||::|||||::|| : | |||| | | |||| ||      | |
Db          1 EVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMHWVRQAPGKGLEWVGYIDPSNGETTY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKL---GTYYFDSWGQGTTLTV 117
              :  |||||:||||:||| |||| |||:||:|:|:| |      | ::|| ||||| :||
Db         61 NQKFKGRFTLSRDNSKNTAYLQMNSLRAEDTAVYYCARGDYRYNGDWFFDVWGQGTLVTV 120

Qy        118 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 180

Qy        178 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 240

Qy        238 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 300

Qy        298 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 360

Qy        358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 417
              :|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 420

Qy        418 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
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Db        421 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 452


RESULT 5
US-09-234-340A-71
; Sequence 71, Application US/09234340A
; Patent No. 6468532
;  GENERAL INFORMATION:
;    APPLICANT:  Genentech, Inc., Hsei, Vanessa
;    APPLICANT:  Koumenis, Iphigenia
;    APPLICANT:  Leong, Steven R.
;    APPLICANT:  Presta, Leonard G.
;    APPLICANT:  Shahrokh, Zahra
```

```
;    APPLICANT:  Zapata, Gerardo A.
;    TITLE OF INVENTION:  METHODS OF TREATING INFLAMMATORY DISEASES
;    TITLE OF INVENTION:  WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
;    NUMBER OF SEQUENCES:  72
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/234,340A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/121,952
;      FILING DATE:  24-Jul-1998
;      APPLICATION NUMBER:  60/074330
;      FILING DATE:  22-JAN-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/075467
;      FILING DATE:  20-FEB-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  P1085R4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-5530
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  71:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  452 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-09-234-340A-71

  Query Match             70.0%;  Score 2149.5;  DB 4;  Length 452;
  Best Local Similarity   88.7%;  Pred. No. 2.6e-159;
  Matches  401;  Conservative   19;  Mismatches   29;  Indels    3;  Gaps    1;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||:|||  |:|||||::||||||:|| : | |||| | | |||| ||      | |
Db          1 EVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMHWVRQAPGKGLEWVGYIDPSNGETTY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKL---GTYYFDSWGQGTTLTV 117
              :  |||||:||||:||| |||| |||:||:|:|:| |      | ::|| ||||| :||
Db         61 NQKFKGRFTLSRDNSKNTAYLQMNSLRAEDTAVYYCARGDYRYNGDWFFDVWGQGTLVTV 120

Qy        118 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 180

Qy        178 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 240

Qy        238 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 300

Qy        298 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 360

Qy        358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 417
              :|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 420

Qy        418 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              ||||||||||||||||||||||||||||||||
Db        421 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 452


RESULT 6
US-08-466-151-8
; Sequence 8, Application US/08466151
; Patent No. 6037453
;  GENERAL INFORMATION:
;    APPLICANT:  Jardieu, Paula M.
;    APPLICANT:  Presta, Leonard G.
;    TITLE OF INVENTION:  Immunoglobulin Variants
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/466,151
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/466163
;      FILING DATE:  06-Jun-1995
;      APPLICATION NUMBER:  08/405617
;      FILING DATE:  15-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/185899
;      FILING DATE:  26-JAN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/879495
;      FILING DATE:  07-MAY-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/744768
;      FILING DATE:  14-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Svoboda, Craig G.
;      REGISTRATION NUMBER:  39,044
;      REFERENCE/DOCKET NUMBER:  P0718P2C1D1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-1489
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  453 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-466-151-8

  Query Match             69.2%;  Score 2124;  DB 3;  Length 453;
  Best Local Similarity   88.8%;  Pred. No. 2.6e-157;
  Matches  403;  Conservative   21;  Mismatches   24;  Indels    6;  Gaps    4;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAF-SHYAMSWVRQTPAKRLEWVAYISSGGSGTY 59
              || ||||||  |:|||||::||| ||::  | |: :|:|| | | ||||| |:  || |
Db          1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGS-TN 59

Qy         60 YSDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVK--LGTYYFDSWGQGTTLTV 117
              |:||||||||||::||| |||| |||:||:|:|:| |      | ::|  ||||| :||
Db         60 YADSVKGRFTISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGTLVTV 119

Qy        118 SSAST--KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 175
              |||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        120 SSASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 179

Qy        176 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE 239

Qy        236 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 299

Qy        296 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 359

Qy        356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 415
              ||:|:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 419

Qy        416 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||||||||||||||||||
Db        420 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 453


RESULT 7
US-08-466-163B-8
; Sequence 8, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
;  APPLICANT: Jardieu, Paula M.
;  APPLICANT:  Presta, Leonard G.
;  TITLE OF INVENTION: Immunoglobulin Variants
;  FILE REFERENCE: P0718P2C1D1
;  CURRENT APPLICATION NUMBER: US/08/466,163B
;  CURRENT FILING DATE:  1995-06-06
;  PRIOR APPLICATION NUMBER: US 08/405,617
;  PRIOR FILING DATE: 1995-03-15
;  PRIOR APPLICATION NUMBER: US 08/185,899
;  PRIOR FILING DATE: 1994-01-26
;  PRIOR APPLICATION NUMBER: US 07/879,495
;  PRIOR FILING DATE: 1992-05-07
;  PRIOR APPLICATION NUMBER: US 07/744,768
;  PRIOR FILING DATE: 1991-08-14
;  NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 8
;   LENGTH: 453
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: humanized maell, version 1 heavy chain
US-08-466-163B-8

  Query Match             69.2%;  Score 2124;  DB 3;  Length 453;
  Best Local Similarity   88.8%;  Pred. No. 2.6e-157;
  Matches  403;  Conservative   21;  Mismatches   24;  Indels    6;  Gaps    4;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAF-SHYAMSWVRQTPAKRLEWVAYISSGGSGTY 59
              || ||||||  |:|||||::||| ||::  | |: :|:|| | | ||||| |:  || |
Db          1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGS-TN 59

Qy         60 YSDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVK--LGTYYFDSWGQGTTLTV 117
              |:|||||||||||::||| |||| |||:||:|:|:| |      | ::|  ||||| :||
Db         60 YADSVKGRFTISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGTLVTV 119

Qy        118 SSAST--KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 175
              |||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 SSASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 179

Qy        176 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE 239

Qy        236 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 299

Qy        296 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 359

Qy        356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 415
              ||:|:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 419

Qy        416 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||||||||||||||||||
Db        420 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 453


RESULT 8
US-09-802-096-8
; Sequence 8, Application US/09802096
; Patent No. 6685939
; GENERAL INFORMATION:
;  APPLICANT:  Jardieu, Paula M.
;  APPLICANT:  Presta, Leonard G.
;  TITLE OF INVENTION:  Method of Preventing the Onset of Allergic Disorders (as amende
;  FILE REFERENCE:  P0718P2C3US
;  CURRENT APPLICATION NUMBER: US/09/802,096
;  CURRENT FILING DATE:  2001-03-08
;  PRIOR APPLICATION NUMBER:  US 08/405,617
;  PRIOR FILING DATE:  1995-03-15
;  PRIOR APPLICATION NUMBER:  US 08/185,899
;  PRIOR FILING DATE:  1994-01-26
;  PRIOR APPLICATION NUMBER:  PCT/US92/06860
;  PRIOR FILING DATE:  1992-08-14
;  PRIOR APPLICATION NUMBER:  US 07/879,495
;  PRIOR FILING DATE:  1992-05-07
;  PRIOR APPLICATION NUMBER:  US 07/744,768
;  PRIOR FILING DATE:  1991-08-14
;  NUMBER OF SEQ ID NOS:  64
; SEQ ID NO 8
;   LENGTH: 453
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: humanized maell, version 1 heavy chain
US-09-802-096-8

  Query Match             69.2%;  Score 2124;  DB 4;  Length 453;
  Best Local Similarity   88.8%;  Pred. No. 2.6e-157;
  Matches  403;  Conservative   21;  Mismatches   24;  Indels    6;  Gaps    4;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAF-SHYAMSWVRQTPAKRLEWVAYISSGGSGTY 59
              || ||||||  |:|||||::||| ||::  | |: :|:|| | | ||||| |:  || |
Db          1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGS-TN 59

Qy         60 YSDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVK--LGTYYFDSWGQGTTLTV 117
              |:|||||||||||::||| |||| |||:||:|:|:| |      | ::|  ||||| :||
Db         60 YADSVKGRFTISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGTLVTV 119

Qy        118 SSAST--KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 175
              |||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 SSASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 179

Qy        176 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE 239

Qy        236 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 299

Qy        296 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 359

Qy        356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 415
              ||:|:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 419

Qy        416 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||||||||||||||||||
Db        420 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 453
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Qy        356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 415
              ||:|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 419

Qy        416 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||||||||||||||||||
Db        420 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 453


RESULT 9
US-09-802-077-8
; Sequence 8, Application US/09802077
; Patent No. 6699472
; GENERAL INFORMATION:
;  APPLICANT: Jardieu, Paula M.
;  APPLICANT:  Presta, Leonard G.
;  TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
;  FILE REFERENCE: P0718P2C2US
;  CURRENT APPLICATION NUMBER: US/09/802,077
;  CURRENT FILING DATE:  2001-03-08
;  PRIOR APPLICATION NUMBER: US 08/405,617
;  PRIOR FILING DATE: 1995-03-15
;  PRIOR APPLICATION NUMBER: US 08/185,899
;  PRIOR FILING DATE: 1994-01-26
;  PRIOR APPLICATION NUMBER: PCT/US92/06860
;  PRIOR FILING DATE: 1992-08-14
;  PRIOR APPLICATION NUMBER: US 07/879,495
;  PRIOR FILING DATE: 1992-05-07
;  PRIOR APPLICATION NUMBER: US 07/744,768
;  PRIOR FILING DATE: 1991-08-14
;  NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 8
;   LENGTH: 453
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: humanized maell, version 1 heavy chain
US-09-802-077-8

  Query Match             69.2%;  Score 2124;  DB 4;  Length 453;
  Best Local Similarity   88.8%;  Pred. No. 2.6e-157;
  Matches  403;  Conservative   21;  Mismatches   24;  Indels    6;  Gaps    4;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAF-SHYAMSWVRQTPAKRLEWVAYISSGGSGTY 59
              || ||||||  |:|||||::||| ||::  | |: :|:|| | | ||||| |:  || |
Db          1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGS-TN 59

Qy         60 YSDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVK--LGTYYFDSWGQGTTLTV 117
              |:|||||||||||::||| |||| |||:||:|:|:| |     | ::|  ||||| :||
Db         60 YADSVKGRFTISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGTLVTV 119

Qy        118 SSAST--KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 175
              |||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 SSASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 179

Qy        176 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE 235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE 239

Qy        236 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 299

Qy        296 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 359

Qy        356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 415
              ||:|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 419

Qy        416 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||||||||||||||||||
Db        420 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 453


RESULT 10
US-08-887-352B-14
; Sequence 14, Application US/08887352B
; Patent No. 5994511
;  GENERAL INFORMATION:
;    APPLICANT:  Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
;    TITLE OF INVENTION:  Improved Anti-IgE Antibodies and Method of
;    TITLE OF INVENTION:  Improving Polypeptides
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/887,352B
;      FILING DATE:  03-Jul-1997
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Svoboda, Craig G.
;      REGISTRATION NUMBER:  39,044
;      REFERENCE/DOCKET NUMBER:  P1123
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-1489
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  451 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-887-352B-14

  Query Match             69.1%;  Score 2122;  DB 2;  Length 451;
  Best Local Similarity   88.7%;  Pred. No. 3.7e-157;
  Matches  401;  Conservative   21;  Mismatches   26;  Indels    4;  Gaps    3;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAF-SHYAMSWVRQTPAKRLEWVAYISSGGSGTY 59
              || ||||||  |:|||||::||| ||::  | |: :|:|| | | ||||| |:  || |
Db          1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGS-TN 59

Qy         60 YSDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVK--LGTYYFDSWGQGTTLTV 117
              |: ||||| ||||||::||| |||| |||:||:|:|:| |     | ::|  ||||| :||
Db         60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGTLVTV 119

Qy        118 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 179

Qy        178 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 239

Qy        238 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 299

Qy        298 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 359

Qy        358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 417
              :|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 419
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Qy        418 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              ||||||||||||||||||||||||||||||||
Db        420 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451


RESULT 11
US-08-887-352B-16
; Sequence 16, Application US/08887352B
; Patent No. 5994511
;  GENERAL INFORMATION:
;    APPLICANT:  Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
;    TITLE OF INVENTION:  Improved Anti-IgE Antibodies and Method of
;    TITLE OF INVENTION:  Improving Polypeptides
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/887,352B
;      FILING DATE:  03-Jul-1997
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Svoboda, Craig G.
;      REGISTRATION NUMBER:  39,044
;      REFERENCE/DOCKET NUMBER:  P1123
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-1489
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  451 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-887-352B-16

  Query Match             69.1%;  Score 2122;  DB 2;  Length 451;
  Best Local Similarity   88.7%;  Pred. No. 3.7e-157;
  Matches  401;  Conservative   21;  Mismatches   26;  Indels    4;  Gaps    3;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAF-SHYAMSWVRQTPAKRLEWVAYISSGGSGTY 59
              || ||||||  |:|||||::||| ||::  | |: :|:|| | | ||||| |:  || |
Db          1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGS-TN 59

Qy         60 YSDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVK--LGTYYFDSWGQGTTLTV 117
              |: ||||| |||||::||| |||| |||:||:|:|:| |      | ::|  ||||| :||
Db         60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGTLVTV 119

Qy        118 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 179

Qy        178 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 239

Qy        238 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 299

Qy        298 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 359

Qy        358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 417
              :|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 419

Qy        418 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              ||||||||||||||||||||||||||||||||
Db        420 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451


RESULT 12
US-08-466-151-65
; Sequence 65, Application US/08466151
; Patent No. 6037453
;  GENERAL INFORMATION:
;    APPLICANT:  Jardieu, Paula M.
;    APPLICANT:  Presta, Leonard G.
;    TITLE OF INVENTION:  Immunoglobulin Variants
;    NUMBER OF SEQUENCES:  65
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/466,151
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/466163
;      FILING DATE:  06-Jun-1995
;      APPLICATION NUMBER:  08/405617
;      FILING DATE:  15-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/185899
;      FILING DATE:  26-JAN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/879495
;      FILING DATE:  07-MAY-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/744768
;      FILING DATE:  14-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Svoboda, Craig G.
;      REGISTRATION NUMBER:  39,044
;      REFERENCE/DOCKET NUMBER:  P0718P2C1D1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-1489
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  65:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  451 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-466-151-65

  Query Match             69.1%;  Score 2122;  DB 3;  Length 451;
  Best Local Similarity   88.7%;  Pred. No. 3.7e-157;
  Matches  401;  Conservative   21;  Mismatches   26;  Indels    4;  Gaps    3;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAF-SHYAMSWVRQTPAKRLEWVAYISSGGSGTY 59
              || ||||||  |:|||||::||| ||::  | |: :|:|| | | ||||| |:  || |
Db          1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGS-TN 59

Qy         60 YSDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVK--LGTYYFDSWGQGTTLTV 117
              |: ||||| |||||::||| |||| |||:||:|:|:| |      | ::|  ||||| :||
Db         60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGTLVTV 119
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Qy        118 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 179

Qy        178 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 239

Qy        238 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 299

Qy        298 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 359

Qy        358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 417
              :|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 419

Qy        418 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
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Db        420 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451
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RESULT 13
US-09-109-207C-14
; Sequence 14, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-14

Query Match 69.1%; Score 2122; DB 3; Length 451;
Best Local Similarity 88.7%; Pred. No. 3.7e-157;
Matches 401; Conservative 21; Mismatches 26; Indels 4; Gaps 3;

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Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAF-SHYAMSWVRQTPAKRLEWVAYISSGGSGTY 59
              || ||||||  |:|||||::||| ||::  | |: :|:|| | | ||||| |:  || |
Db          1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGS-TN 59

Qy         60 YSDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVK--LGTYYFDSWGQGTTLTV 117
              |: ||||| |||||::||| |||| ||||:||:|:|:| |     | ::|  ||||| :||
Db         60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGTLVTV 119

Qy        118 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 179

Qy        178 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 239

Qy        238 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 299
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Qy        298 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 359

Qy        358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 417
              :|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 419

Qy        418 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              ||||||||||||||||||||||||||||||||
Db        420 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451
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RESULT 14
US-09-109-207C-16
; Sequence 16, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 16
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-16

Query Match 69.1%; Score 2122; DB 3; Length 451;
Best Local Similarity 88.7%; Pred. No. 3.7e-157;
Matches 401; Conservative 21; Mismatches 26; Indels 4; Gaps 3;

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Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAF-SHYAMSWVRQTPAKRLEWVAYISSGGSGTY 59
              || ||||||  |:|||||::||| ||::  | |: :|:|| | | ||||| |:  || |
Db          1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGS-TN 59

Qy         60 YSDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVK--LGTYYFDSWGQGTTLTV 117
              |: ||||| |||||::||| |||| ||||:||:|:|:| |     | ::|  ||||| :||
Db         60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGTLVTV 119

Qy        118 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 179

Qy        178 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 239

Qy        238 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 299

Qy        298 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 357
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Db        300 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 359

Qy        358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 417
              :|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 419

Qy        418 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
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Db        420 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451
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RESULT 15
US-09-296-005-14
; Sequence 14, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
;  APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
;  TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
;  FILE REFERENCE: P1123C1r
;  CURRENT APPLICATION NUMBER: US/09/296,005
;  CURRENT FILING DATE: 1999-04-21
;  EARLIER APPLICATION NUMBER: US 08/887,352
;  EARLIER FILING DATE: 1997-07-02
;  NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 14
;   LENGTH: 451
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   NAME/KEY: Artificial
;   LOCATION: 1-451
;   OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-296-005-14

  Query Match             69.1%;  Score 2122;  DB 3;  Length 451;
  Best Local Similarity   88.7%;  Pred. No. 3.7e-157;
  Matches  401;  Conservative   21;  Mismatches   26;  Indels    4;  Gaps    3;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAF-SHYAMSWVRQTPAKRLEWVAYISSGGSGTY 59
              || ||||||  |:|||||::||| ||::  | |: :|:|| | | ||||| |:  || |
Db          1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGS-TN 59

Qy         60 YSDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVK--LGTYYFDSWGQGTTLTV 117
              |:.||||| |||||::||| |||| |||:||:|:|:|:| |     | ::|  ||||| :||
Db         60 YNPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGTLVTV 119

Qy        118 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 179

Qy        178 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 239

Qy        238 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 299

Qy        298 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 359

Qy        358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 417
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Db        360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 419

Qy        418 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
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Db        420 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451


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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

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(without alignments)
1578.640 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

Searched: 1595201 seqs, 359116952 residues

Total number of hits satisfying chosen parameters: 1595201

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2744.5	89.4	579	14	US-10-138-727A-41	Sequence 41, Appl
2	2738.5	89.2	579	14	US-10-310-719-32	Sequence 32, Appl
3	2715.5	88.4	575	17	US-10-737-208A-6	Sequence 6, Appli
4	2592	84.4	580	14	US-10-310-719-37	Sequence 37, Appl
5	2560	83.4	580	14	US-10-310-719-35	Sequence 35, Appl
6	2218.5	72.2	663	15	US-10-412-406-32	Sequence 32, Appl
7	2218.5	72.2	4852	15	US-10-412-406-33	Sequence 33, Appl
8	2216	72.2	713	16	US-10-679-620-64	Sequence 64, Appl
9	2216	72.2	715	16	US-10-679-620-62	Sequence 62, Appl
10	2201.5	71.7	447	15	US-10-474-832-4	Sequence 4, Appli
11	2200.5	71.7	444	14	US-10-150-475A-6	Sequence 6, Appli
12	2200.5	71.7	444	16	US-10-704-522-6	Sequence 6, Appli
13	2200.5	71.7	444	16	US-10-645-215-6	Sequence 6, Appli
14	2197	71.5	449	17	US-10-635-908-16	Sequence 16, Appl
15	2197	71.5	449	17	US-10-635-908-18	Sequence 18, Appl
16	2195.5	71.5	445	14	US-10-320-231A-79	Sequence 79, Appl
17	2195.5	71.5	447	15	US-10-474-832-5	Sequence 5, Appli
18	2191.5	71.4	447	15	US-10-474-832-6	Sequence 6, Appli
19	2184.5	71.1	446	15	US-10-408-901-38	Sequence 38, Appl
20	2181	71.0	449	9	US-09-736-371B-21	Sequence 21, Appl
21	2181	71.0	449	15	US-10-463-442-21	Sequence 21, Appl
22	2181	71.0	474	10	US-09-848-832-3	Sequence 3, Appli
23	2181	71.0	474	14	US-10-225-108A-3	Sequence 3, Appli
24	2181	71.0	474	15	US-10-461-148-1	Sequence 1, Appli
25	2177.5	70.9	442	15	US-10-226-435A-12	Sequence 12, Appl
26	2177.5	70.9	442	17	US-10-487-326-12	Sequence 12, Appl
27	2177.5	70.9	442	17	US-10-486-908-12	Sequence 12, Appl
28	2177.5	70.9	477	14	US-10-291-265-395	Sequence 395, App
29	2176	70.9	445	15	US-10-408-901-34	Sequence 34, Appl
30	2171	70.7	451	9	US-09-822-698A-26	Sequence 26, Appl
31	2170.5	70.7	442	17	US-10-487-322-12	Sequence 12, Appl
32	2170.5	70.7	442	17	US-10-487-326-21	Sequence 21, Appl
33	2170.5	70.7	442	17	US-10-486-908-16	Sequence 16, Appl
34	2166.5	70.5	446	15	US-10-408-901-46	Sequence 46, Appl
35	2166.5	70.5	469	17	US-10-858-186-14	Sequence 14, Appl
36	2159.5	70.3	446	15	US-10-408-901-30	Sequence 30, Appl
37	2159	70.3	445	15	US-10-408-901-42	Sequence 42, Appl
38	2158.5	70.3	446	15	US-10-408-901-50	Sequence 50, Appl
39	2153.5	70.1	469	15	US-10-656-769-26	Sequence 26, Appl
40	2152	70.1	474	15	US-10-108-260A-4640	Sequence 4640, Ap
41	2149.5	70.0	452	10	US-09-726-258-71	Sequence 71, Appl
42	2147.5	69.9	469	15	US-10-656-769-20	Sequence 20, Appl
43	2145.5	69.9	447	16	US-10-379-392-116	Sequence 116, App
44	2145.5	69.9	452	17	US-10-818-765-4	Sequence 4, Appli
45	2144.5	69.8	447	16	US-10-379-392-117	Sequence 117, App

ALIGNMENTS

```
RESULT 1
US-10-138-727A-41
; Sequence 41, Application US/10138727A
; Publication No. US20030157054A1
; GENERAL INFORMATION:
;  APPLICANT: Gillies, Stephen
;  APPLICANT:  Lo, Kin-Ming
;  APPLICANT:  Qian, Susan
;  TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
;  FILE REFERENCE: LEX-019
;  CURRENT APPLICATION NUMBER: US/10/138,727A
;  CURRENT FILING DATE:  2002-05-03
;  PRIOR APPLICATION NUMBER: US 60/288,564
;  PRIOR FILING DATE: 2001-05-03
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 41
;   LENGTH: 579
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: heavy chain-IL2
US-10-138-727A-41

  Query Match             89.4%;  Score 2744.5;  DB 14;  Length 579;
  Best Local Similarity   88.5%;  Pred. No. 1.4e-166;
  Matches  516;  Conservative   31;  Mismatches   31;  Indels    5;  Gaps    2;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              :: ||:|| :  ||| ::|:|| |||: |::| |:|||||| | |:|: :|::      |
Db          1 QIQLVQSGAEVKKPGETVKISCKASGYTFTNYGMNWVKQTPGKGLKWMGWINTYTGEPTY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTR-VKLGTYYFDSWGQGTTLTVSS 119
              :|  ||||  | : : :| :||: :|||||:| ||| | :  | |    |||||::||||
Db         61 ADDFKGRFAFSLETSTSTAFLQINNLRSEDTATYFCVRFISKGDY----WGQGTSVTVSS 116
```

```
Qy        120 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        117 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 176

Qy        180 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 239
              ||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||||
Db        177 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGG 236

Qy        240 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        237 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 296

Qy        300 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db        297 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE 356

Qy        360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 419
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        357 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 416

Qy        420 QQGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMILNGINN 479
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        417 QQGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMILNGINN 476

Qy        480 YKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNIN 539
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        477 YKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNIN 536

Qy        540 VIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 582
              |||||||||||||||||||||||||||||||||||||||||||
Db        537 VIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 579
```

RESULT 2
US-10-310-719-32
; Sequence 32, Application US/10310719
; Publication No. US20030166163A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Immunocytokines With Modulated Selectivity
; FILE REFERENCE: LEX-020
; CURRENT APPLICATION NUMBER: US/10/310,719
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,113
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/371,966
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: dI-KS-ala IL2 (D20T) heavy chain fused to IL-2 variant
US-10-310-719-32

Query Match 89.2%; Score 2738.5; DB 14; Length 579;
Best Local Similarity 88.3%; Pred. No. 3.3e-166;
Matches 515; Conservative 30; Mismatches 33; Indels 5; Gaps 2;

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Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              :: ||:|| :  ||| |:|:|| |||: |::| |:|||| | | |:|: :|::      |
Db          1 QIQLVQSGPELKKPGSSVKISCKASGYTFTNYGMNWVRQAPGKGLKWMGWINTYTGEPTY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTR-VKLGTYYFDSWGQGTTLTVSS 119
              :|  ||||||: : : :|||||: :|||||:| ||| | :  | |    ||||||:||||
Db         61 ADDFKGRFTITAETSTSTLYLQLNNLRSEDTATYFCVRFISKGDY----WGQGTTVTVSS 116

Qy        120 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        117 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 176
```

```
Qy        180 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 239
              ||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||||
Db        177 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGG 236

Qy        240 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        237 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 296

Qy        300 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db        297 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE 356

Qy        360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 419
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        357 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 416

Qy        420 QQGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMILNGINN 479
              |||||||||||||||||||||| : :|| |||||||||||||||||| ||||||||||
Db        417 QQGNVFSCSVMHEALHNHYTQKSATATPGAAPTSSSTKKTQLQLEHLLLTLQMILNGINN 476

Qy        480 YKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNIN 539
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        477 YKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNIN 536

Qy        540 VIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 582
              |||||||||||||||||||||||||||||||||||||||||||
Db        537 VIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 579
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RESULT 3
US-10-737-208A-6
; Sequence 6, Application US/10737208A
; Publication No. US20040203100A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen D.
; APPLICANT: Lo, Kin-Ming
; TITLE OF INVENTION: IMMUNOCYTOKINE SEQUENCES AND USES THEREOF
; FILE REFERENCE: LEX-023
; CURRENT APPLICATION NUMBER: US/10/737,208A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 60/433,945
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized Immunoglobulin Heavy Chain-IL-2
US-10-737-208A-6

Query Match 88.4%; Score 2715.5; DB 17; Length 575;
Best Local Similarity 88.8%; Pred. No. 9.5e-165;
Matches 517; Conservative 24; Mismatches 34; Indels 7; Gaps 3;

```
Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||:|| :  ||| |:|:|| ||| :|: | |:||||   | |||:  |     || |
Db          1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSSA 120
              :   ||| |:: | : :| |: ::||||||:|:|:|     |  |   |||||::|||||
Db         61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDTAVYYCVS---GMEY---WGQGTSVTVSSA 114

Qy        121 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 174

Qy        181 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 240
              ||||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||
Db        175 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGP 234

Qy        241 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300
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Qy        359 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 418
              |:||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db        357 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSR 416

Qy        419 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLLDLQMILNGIN 478
              |||||||||||||||||||||| : :|| |||||||||||||||||| |||||||||
Db        417 WQQGNVFSCSVMHEALHNHYTQKSATATPGAAPTSSSTKKTQLQLEHLLLTLQMILNGIN 476

Qy        479 NYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNI 538
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        477 NYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNI 536

Qy        539 NVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 582
              |||||||||||||||||||||||||||||||||||||||||||
Db        537 NVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT 580
```

RESULT 6
US-10-412-406-32
; Sequence 32, Application US/10412406
; Publication No. US20040058394A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; APPLICANT: GARBER, Ellen
; APPLICANT: LYNE, Paul
; APPLICANT: SALDHANA, Jose W.
; TITLE OF INVENTION: HUMANIZED ANTI-LT-BETA-R ANTIBODIES
; FILE REFERENCE: BINA100CN
; CURRENT APPLICATION NUMBER: US/10/412,406
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: 60/240,285
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/275,289
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/299,987
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: PCT/US01/32140
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-412-406-32

Query Match 72.2%; Score 2218.5; DB 15; Length 663;
Best Local Similarity 93.1%; Pred. No. 5.2e-133;
Matches 418; Conservative 9; Mismatches 21; Indels 1; Gaps 1;

```
Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||  |||||||::||||||| || | | | || | | ||||| || ||| |||
Db        215 EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMYWFRQAPGKGLEWVATISDGGSYTYY 274

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGT-YYFDSWGQGTTLTVSS 119
               |||||||||||||||:||||| |||:||:|:|:| | : |  |||| ||||||:||||
Db        275 PDSVKGRFTISRDNAKNSLYLQMSSLRAEDTAVYYCAREENGNFYYFDYWGQGTTVTVSS 334

Qy        120 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        335 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 394

Qy        180 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        395 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 454

Qy        240 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        455 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 514

Qy        300 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        515 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 574

Qy        360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 419
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        575 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 634

Qy        420 QQGNVFSCSVMHEALHNHYTQKSLSLSPG 448
              |||||||||||||||||||||||||||||
Db        635 QQGNVFSCSVMHEALHNHYTQKSLSLSPG 663
```

RESULT 7
US-10-412-406-33
; Sequence 33, Application US/10412406
; Publication No. US20040058394A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; APPLICANT: GARBER, Ellen
; APPLICANT: LYNE, Paul
; APPLICANT: SALDHANA, Jose W.
; TITLE OF INVENTION: HUMANIZED ANTI-LT-BETA-R ANTIBODIES
; FILE REFERENCE: BINA100CN
; CURRENT APPLICATION NUMBER: US/10/412,406
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: 60/240,285
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/275,289
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/299,987
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: PCT/US01/32140
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 4852
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-412-406-33

Query Match 72.2%; Score 2218.5; DB 15; Length 4852;
Best Local Similarity 93.1%; Pred. No. 5.4e-132;
Matches 418; Conservative 9; Mismatches 21; Indels 1; Gaps 1;

```
Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||  |||||||::||||||| || | | | || | | ||||| || ||| |||
Db       4404 EVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMYWFRQAPGKGLEWVATISDGGSYTYY 4463

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGT-YYFDSWGQGTTLTVSS 119
               |||||||||||||||:||||| |||:||:|:|:| | : |  |||| ||||||:||||
Db       4464 PDSVKGRFTISRDNAKNSLYLQMSSLRAEDTAVYYCAREENGNFYYFDYWGQGTTVTVSS 4523

Qy        120 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4524 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 4583

Qy        180 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4584 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 4643

Qy        240 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4644 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 4703

Qy        300 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4704 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 4763

Qy        360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 419
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4764 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 4823

Qy        420 QQGNVFSCSVMHEALHNHYTQKSLSLSPG 448
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                     ||||||||||||||||||||||||||||||
Db       4824 QQGNVFSCSVMHEALHNHYTQKSLSLSPG 4852


RESULT 8
US-10-679-620-64
; Sequence 64, Application US/10679620
; Publication No. US20040110930A1
; GENERAL INFORMATION:
;  APPLICANT: Large Scale Biology
;  APPLICANT:  Reinl, Stephen J.
;  APPLICANT:  Edwards, Patricia C.
;  TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
;  FILE REFERENCE: 34150-004A
;  CURRENT APPLICATION NUMBER: US/10/679,620
;  CURRENT FILING DATE:  2003-10-03
;  PRIOR APPLICATION NUMBER: 60/415,940
;  PRIOR FILING DATE: 2002-10-03
;  NUMBER OF SEQ ID NOS: 122
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 64
;   LENGTH: 713
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: p9E10chimericv2-1, see Example 15
US-10-679-620-64

  Query Match             72.2%;  Score 2216;  DB 16;  Length 713;
  Best Local Similarity   91.7%;  Pred. No. 8.2e-133;
  Matches  419;  Conservative   10;  Mismatches   20;  Indels    8;  Gaps    2;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||| |||||||:|||||| |||| |||||||| ||||||| | | |: |:|
Db        257 EVDLVESGGDLVKPGGSLKLSCAASGFTFSHYGMSWVRQTPDKRLEWVATIGSRGTYTHY 316

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKL-----GTYYF---DSWGQG 112
              |||||||||||| || ||||| ||:|||:|||:| |         |||:    | ||||
Db        317 PDSVKGRFTISRDNDKNALYLQMNSLKSEDTAMYYCARRSEFYYYGNTYYYSAMDYWGQG 376

Qy        113 TTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 172
              ::|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 ASVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 436

Qy        173 PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCP 232
              ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||
Db        437 PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP 496

Qy        233 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        497 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 556

Qy        293 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        557 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT 616

Qy        353 LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL 412
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        617 LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL 676

Qy        413 TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||||||||||||||||||||||
Db        677 TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 713


RESULT 9
US-10-679-620-62
; Sequence 62, Application US/10679620
; Publication No. US20040110930A1
; GENERAL INFORMATION:
;  APPLICANT: Large Scale Biology
;  APPLICANT:  Reinl, Stephen J.
;  APPLICANT:  Edwards, Patricia C.
;  TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
;  FILE REFERENCE: 34150-004A
;  CURRENT APPLICATION NUMBER: US/10/679,620
;  CURRENT FILING DATE:  2003-10-03
;  PRIOR APPLICATION NUMBER: 60/415,940
;  PRIOR FILING DATE: 2002-10-03
;  NUMBER OF SEQ ID NOS: 122
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
;   LENGTH: 715
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: p9E10chimericv1-1, see Example 15
US-10-679-620-62

  Query Match             72.2%;  Score 2216;  DB 16;  Length 715;
  Best Local Similarity   91.7%;  Pred. No. 8.3e-133;
  Matches  419;  Conservative   10;  Mismatches   20;  Indels    8;  Gaps    2;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||| |||||||:|||||| |||| |||||||| ||||||| | | |: |:|
Db        259 EVDLVESGGDLVKPGGSLKLSCAASGFTFSHYGMSWVRQTPDKRLEWVATIGSRGTYTHY 318

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKL-----GTYYF---DSWGQG 112
              |||||||||||| || ||||| ||:|||:|||:| |         |||:    | ||||
Db        319 PDSVKGRFTISRDNDKNALYLQMNSLKSEDTAMYYCARRSEFYYYGNTYYYSAMDYWGQG 378

Qy        113 TTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 172
              ::|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 ASVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 438

Qy        173 PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCP 232
              ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||
Db        439 PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP 498

Qy        233 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 558

Qy        293 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT 618

Qy        353 LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL 412
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL 678

Qy        413 TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||||||||||||||||||||||
Db        679 TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 715


RESULT 10
US-10-474-832-4
; Sequence 4, Application US/10474832
; Publication No. US20040081651A1
; GENERAL INFORMATION:
;  APPLICANT: BIOGEN, INC.
;  TITLE OF INVENTION: ANTIBODIES TO VLA-1
;  FILE REFERENCE: A101 PCT
;  CURRENT APPLICATION NUMBER: US/10/474,832
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: 60/283,794
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/303,689
;  PRIOR FILING DATE: 2001-07-06
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 447
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
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```
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: polypeptide
US-10-474-832-4

  Query Match             71.7%;  Score 2201.5;  DB 15;  Length 447;
  Best Local Similarity   92.9%;  Pred. No. 4e-132;
  Matches  416;  Conservative    9;  Mismatches   22;  Indels    1;  Gaps    1;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||  |:|||||::|||||| || | |||||| | | ||||| || ||  |||
Db          1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSRYTMSWVRQAPGKGLEWVATISGGGH-TYY 59

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSSA 120
              |||||||||||||:|||||||| |||:||:|:|:|||      ||| ||||| :|||||
Db         60 LDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCTRGFGDGGYFDVWGQGTLVTVSSA 119

Qy        121 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 179

Qy        181 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 239

Qy        241 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 299

Qy        301 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 359

Qy        361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 419

Qy        421 QGNVFSCSVMHEALHNHYTQKSLSLSPG 448
              ||||||||||||||||||||||||||||
Db        420 QGNVFSCSVMHEALHNHYTQKSLSLSPG 447


RESULT 11
US-10-150-475A-6
; Sequence 6, Application US/10150475A
; Publication No. US20030103985A1
; GENERAL INFORMATION:
;  APPLICANT: Adolf, G. et al.
;  TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates
;  FILE REFERENCE: 1/1211
;  CURRENT APPLICATION NUMBER: US/10/150,475A
;  CURRENT FILING DATE:  2002-05-17
;  PRIOR APPLICATION NUMBER: US 60/307,451
;  PRIOR FILING DATE: 2001-07-24
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 444
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Humanised
;   OTHER INFORMATION: Murine Antibody BIWA 4 Heavy Chain SEQ ID NO: 6
US-10-150-475A-6

  Query Match             71.7%;  Score 2200.5;  DB 14;  Length 444;
  Best Local Similarity   92.4%;  Pred. No. 4.6e-132;
  Matches  415;  Conservative   11;  Mismatches   18;  Indels    5;  Gaps    1;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||  |||||||::||||||| || | |||||| | | |||: |||||| |||
Db          1 EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVSTISSGGSYTYY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSSA 120
              ||:|||||||||||:||||| |||:||:|:|:|| |  |     | ||:|| :|||||
Db         61 LDSIKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARQGL-----DYWGRGTLVTVSSA 115

Qy        121 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        116 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 175

Qy        181 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        176 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 235

Qy        241 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        236 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 295

Qy        301 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 355

Qy        361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        356 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 415

Qy        421 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||||||||||||||
Db        416 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 444


RESULT 12
US-10-704-522-6
; Sequence 6, Application US/10704522
; Publication No. US20040120949A1
; GENERAL INFORMATION:
;  APPLICANT: Adolf, Gunther
;  APPLICANT:  Baumann, Michael
;  APPLICANT:  Heider, Karl-Heinz
;  TITLE OF INVENTION: Compositions and methods for treating cancer using
;  TITLE OF INVENTION:  cytotoxic CD44 Antibody Immunoconjugates
;  FILE REFERENCE: 1/1414
;  CURRENT APPLICATION NUMBER: US/10/704,522
;  CURRENT FILING DATE:  2003-11-07
;  PRIOR APPLICATION NUMBER: US 60/429,516
;  PRIOR FILING DATE: 2002-11-27
;  PRIOR APPLICATION NUMBER: EP 02024881
;  PRIOR FILING DATE: 2002-11-08
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 444
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Heavy Chain
US-10-704-522-6

  Query Match             71.7%;  Score 2200.5;  DB 16;  Length 444;
  Best Local Similarity   92.4%;  Pred. No. 4.6e-132;
  Matches  415;  Conservative   11;  Mismatches   18;  Indels    5;  Gaps    1;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||  |||||||::||||||| || | |||||| | | ||||: |||||| |||
Db          1 EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVSTISSGGSYTYY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSSA 120
              ||:|||||||||||:||||| |||:||:|:|:|| |  |     | ||:|| :|||||
Db         61 LDSIKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARQGL-----DYWGRGTLVTVSSA 115

Qy        121 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        116 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 175

Qy        181 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 240
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Db        176 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 235

Qy        241 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300

Db        236 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 295

Qy        301 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360

Db        296 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 355

Qy        361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 420

Db        356 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 415

Qy        421 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 449

Db        416 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 444
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RESULT 13
US-10-645-215-6
; Sequence 6, Application US/10645215
; Publication No. US20040126379A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Guenther
; APPLICANT: Baum, Anke
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates and
; TITLE OF INVENTION: Chemotherapeutic Agents
; FILE REFERENCE: 1/1383
; CURRENT APPLICATION NUMBER: US/10/645,215
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: EP 02 018 686.2
; PRIOR FILING DATE: August 21, 2002
; PRIOR APPLICATION NUMBER: US 60/405,956
; PRIOR FILING DATE: August 26, 2002
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Heavy Chain
US-10-645-215-6

Query Match 71.7%; Score 2200.5; DB 16; Length 444;
Best Local Similarity 92.4%; Pred. No. 4.6e-132;
Matches 415; Conservative 11; Mismatches 18; Indels 5; Gaps 1;

```
Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60

Db          1 EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVSTISSGGSYTYY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSSA 120

Db         61 LDSIKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARQGL-----DYWGRGTLVTVSSA 115

Qy        121 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180

Db        116 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 175

Qy        181 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 240

Db        176 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 235

Qy        241 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300

Db        236 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 295

Qy        301 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360

Db        296 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 355

Qy        361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 420

Db        356 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 415

Qy        421 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 449

Db        416 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 444
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RESULT 14
US-10-635-908-16
; Sequence 16, Application US/10635908
; Publication No. US20040219633A1
; GENERAL INFORMATION:
; APPLICANT: Bolhuis, Reinier LH
; APPLICANT: Woehl, Thorsten
; APPLICANT: Boettger , Volker
; TITLE OF INVENTION: Method of Producing Recombinant Antibodies
; FILE REFERENCE: 2923-552
; CURRENT APPLICATION NUMBER: US/10/635,908
; CURRENT FILING DATE: 2003-08-07
; PRIOR APPLICATION NUMBER: PCT/EP02/01283
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 60/327,008
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/266,853
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: mouse anti-human monoclonal antibody
US-10-635-908-16

Query Match 71.5%; Score 2197; DB 17; Length 449;
Best Local Similarity 92.2%; Pred. No. 7.8e-132;
Matches 414; Conservative 14; Mismatches 21; Indels 0; Gaps 0;

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Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60

Db          1 DVKLVESGGGLVKLGGSLKLSCAASGFTFSNYYMSWVRQTPEKRLELVAAINSDGGITYY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSSA 120

Db         61 LDTVKGRFTISRDNAKNTLYLQMSSLKSEDTALFYCARHRSGYFSMDYWGQGTSVTVSSA 120

Qy        121 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180

Db        121 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180

Qy        181 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 240

Db        181 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 240

Qy        241 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300

Db        241 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300

Qy        301 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360

Db        301 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360

Qy        361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 420

Db        361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 420

Qy        421 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
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                ||||||||||||||||||||||||||||||
Db        421 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 449


RESULT 15
US-10-635-908-18
; Sequence 18, Application US/10635908
; Publication No. US20040219633A1
; GENERAL INFORMATION:
;  APPLICANT: Bolhuis, Reinier LH
;  APPLICANT:  Woehl, Thorsten
;  APPLICANT:  Boettger , Volker
;  TITLE OF INVENTION: Method of Producing Recombinant Antibodies
;  FILE REFERENCE: 2923-552
;  CURRENT APPLICATION NUMBER: US/10/635,908
;  CURRENT FILING DATE:  2003-08-07
;  PRIOR APPLICATION NUMBER: PCT/EP02/01283
;  PRIOR FILING DATE: 2002-02-07
;  PRIOR APPLICATION NUMBER: 60/327,008
;  PRIOR FILING DATE: 2001-10-05
;  PRIOR APPLICATION NUMBER: 60/266,853
;  PRIOR FILING DATE: 2001-02-07
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
;   LENGTH: 449
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: mouse anti-human monoclonal antibody
US-10-635-908-18

  Query Match             71.5%;  Score 2197;  DB 17;  Length 449;
  Best Local Similarity   92.2%;  Pred. No. 7.8e-132;
  Matches  414;  Conservative   14;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              :| ||||||  || |||||:||||||| ||:| |||||||| |||| || |:| |  |||
Db          1 DVKLVESGGGLVKLGGSLKLSCAASGFTFSNYYMSWVRQTPEKRLELVAAINSDGGITYY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSSA 120
               |:|||||||||||||||||| ||:|||:|:::| | : | :  | |||||::|||||
Db         61 LDTVKGRFTISRDNAKNTLYLQMSSLKSEDTALFYCARHRSGYFSMDYWGQGTSVTVSSA 120

Qy        121 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180

Qy        181 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGP 240

Qy        241 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 300

Qy        301 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360

Qy        361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 420

Qy        421 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              ||||||||||||||||||||||||||||
Db        421 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 449


Search completed: December 23, 2004, 19:35:51
Job time : 133.396 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2004, 18:46:03 ; Search time 31.449 Seconds
(without alignments)
1780.604 Million cell updates/sec

Title: US-10-089-500-57
Perfect score: 3071
Sequence: 1 EVTLVESGGDFVKPGGSLKV.....IVEFLNRWITFCQSIISTLT 582

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1767	57.5	330	1	GHHU	Ig gamma-1 chain C
2	1630.5	53.1	377	2	A23511	Ig gamma-3 chain C
3	1628.5	53.0	377	2	A60764	Ig gamma-3 chain C
4	1604	52.2	326	1	G2HU	Ig gamma-2 chain C
5	1590.5	51.8	327	1	G4HU	Ig gamma-4 chain C
6	1507.5	49.1	444	2	PC4436	monoclonal antibod
7	1466	47.7	470	2	S22080	Ig heavy chain pre
8	1430.5	46.6	469	2	S37483	Ig gamma-2a chain
9	1423	46.3	374	2	S69339	Ig heavy chain V r
10	1421	46.3	446	2	S40295	Ig gamma-2a chain
11	1412	46.0	472	2	S31459	Ig gamma-1 chain -
12	1365	44.4	474	1	G2MS11	Ig gamma-2b chain
13	1343.5	43.7	475	2	S01321	Ig gamma-2b chain
14	1263	41.1	328	2	I47159	Ig gamma 2a chain
15	1260	41.0	255	4	S31866	Ig gamma-1 chain C
16	1257	40.9	328	2	I47160	Ig gamma 2b chain
17	1254	40.8	234	2	PT0207	Ig gamma chain C r
18	1231	40.1	328	2	I47158	Ig gamma 1 chain c
19	1230.5	40.1	323	1	GHRB	Ig gamma chain C r
20	1227	40.0	328	2	I47161	Ig gamma 3 chain c
21	1216.5	39.6	329	1	G2GP	Ig gamma-2 chain C
22	1161.5	37.8	308	2	C30554	Ig heavy chain C r
23	1152	37.5	326	2	PS0017	Ig gamma-1 chain C
24	1151	37.5	289	1	G3HUWI	Ig gamma-3 heavy c
25	1146.5	37.3	333	2	PS0018	Ig gamma-2b chain
26	1142	37.2	324	1	G1MS	Ig gamma-1 chain C
27	1141	37.2	329	1	G3MSC	Ig gamma-3 chain C
28	1139	37.1	393	1	G1MSM	Ig gamma-1 chain C
29	1130	36.8	398	1	G3MSM	Ig gamma-3 chain C
30	1126	36.7	330	1	G2MSA	Ig gamma-2a chain
31	1123.5	36.6	335	1	G2MSAB	Ig gamma-2a chain
32	1121	36.5	399	1	G2MSAM	Ig gamma-2a chain
33	1118.5	36.4	329	2	S00847	Ig gamma-2c chain
34	1118	36.4	548	2	S38864	Ig epsilon chain C
35	1112	36.2	322	2	PS0019	Ig gamma-2a chain
36	1092.5	35.6	327	2	S06611	Ig gamma-2 chain C
37	1082	35.2	405	1	G2MSBM	Ig gamma-2b chain
38	1066	34.7	277	2	I47162	Ig gamma 4 chain c
39	845.5	27.5	549	2	S04845	Ig heavy chain pre
40	817.5	26.6	249	2	S69340	Ig heavy chain VHI
41	802.5	26.1	572	2	B46529	Ig Y heavy chain (
42	801.5	26.1	241	2	S69131	Ig heavy chain (DO
43	770	25.1	218	2	A36040	Ig heavy chain V-I
44	760	24.7	220	2	A49444	Ig gamma-1 heavy c
45	744.5	24.2	254	2	B31790	Ig heavy chain V r

ALIGNMENTS

RESULT 1
GHHU
Ig gamma-1 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C;Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
R;Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A;Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A;Reference number: A93433; MUID:82274238; PMID:6287432
A;Accession: A93433
A;Molecule type: DNA
A;Residues: 1-330 <ELL>
A;Cross-references: UNIPROT:P01857; EMBL:Z17370
A;Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers,
A;Note: Lys-330 is removed after translation
R;Harris, L.J.
submitted to the EMBL Data Library, October 1992
A;Reference number: S33904
A;Accession: S36861
A;Molecule type: DNA
A;Residues: 2-330 <HAR>
A;Cross-references: EMBL:Z17370
R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
A;Reference number: S33887; MUID:83001943; PMID:6811139
A;Accession: S33887
A;Molecule type: DNA
A;Residues: 88-113;235-330 <TAK>
A;Cross-references: EMBL:Z17370
R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,
Biochemistry 9, 3161-3170, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seque
A;Reference number: A90563; MUID:71064024; PMID:5489771
A;Contents: myeloma protein Eu
A;Accession: B90563
A;Molecule type: protein
A;Residues: 1-96,'R',98-135 <CUN>
A;Note: this sequence has the G1m(3) marker, 97-Arg
R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequ
A;Reference number: A90564; MUID:71064025; PMID:5530842
A;Contents: Eu
A;Accession: A90564
A;Molecule type: protein
A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240
A;Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met
R;Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A;Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie)

igen Primaerstruktur.
A;Reference number: A91668; MUID:77070269; PMID:826475
A;Contents: myeloma protein Nie
A;Accession: B91668
A;Molecule type: protein
A;Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',27
A;Note: this sequence has the G1m(17) and G1m(1) markers
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A;Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KOL
A;Reference number: A91723; MUID:83289131; PMID:6884994
A;Contents: myeloma protein KOL; disulfide bonds
A;Accession: A91723
A;Molecule type: protein
A;Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SCH
A;Note: this sequence has the G1m(3) and G1m(non-1) markers
R;Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A;Reference number: A90565; MUID:71064027; PMID:4923144
A;Contents: annotation; disulfide bonds
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enbromide cleavage products, and the disulfide bridges.
A;Reference number: A91667; MUID:77070267; PMID:1002129
A;Contents: annotation; disulfide bonds
C;Genetics:
A;Gene: GDB:IGHG1
A;Cross-references: GDB:120085; OMIM:147100
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 114/1; 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;137-206/Domain: immunoglobulin homology <IM2>
F;243-310/Domain: immunoglobulin homology <IM3>
F;27-83,144-204,250-308/Disulfide bonds: #status experimental
F;103/Disulfide bonds: interchain (to light chain) #status experimental
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental

  Query Match 57.5%; Score 1767; DB 1; Length 330;
  Best Local Similarity 100.0%; Pred. No. 2.6e-92;
  Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        120 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy        180 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120

Qy        240 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

Qy        300 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

Qy        360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 419
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300

Qy        420 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||||||||||||||
Db        301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
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RESULT 2
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C;Accession: A23511
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: cc
A;Reference number: A23511; MUID:86148507; PMID:3081877
A;Accession: A23511
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C;Genetics:
A;Gene: GDB:IGHG3
A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

  Query Match 53.1%; Score 1630.5; DB 2; Length 377;
  Best Local Similarity 82.0%; Pred. No. 1.4e-84;
  Matches 309; Conservative 10; Mismatches 11; Indels 47; Gaps 1;

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Qy        120 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
              |||||||||||||| :||||||||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy        180 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV---------------------- 217
              |||||||||||||||||||| |||||||||||||||:|
Db         61 GLYSLSSVVTVPSSSLGTQTYTCNVNHKPSNTKVDKRVELKTPLGDTTHTCPRCPEPKSC 120

Qy        218 -------------------------EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDT 252
                                      ||||||    || ||||||||||||||||||||||
Db        121 DTPPPCPRCPEPKSCDTPPPCPRCPEPKSCDTPPPCPRCPAPELLGGPSVFLFPPKPKDT 180

Qy        253 LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH 312
              |||||||||||||||||||||||:| ||||||||||||||||||:||||||||||
Db        181 LMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQYNSTFRVVSVLTVLH 240

Qy        313 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK 372
              |||||||||||||||||||||||||||| ||||||||||||||:|:||||||||||||
Db        241 QDWLNGKEYKCKVSNKALPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVK 300

Qy        373 GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE 432
              |||||||||||||:||||||| ||||:||||||||||||||||||||:||||||||
Db        301 GFYPSDIAVEWESSGQPENNYNTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHE 360

Qy        433 ALHNHYTQKSLSLSPGK 449
              |||| :||||||||||||
Db        361 ALHNRFTQKSLSLSPGK 377
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RESULT 3
A60764
Ig gamma-3 chain C region, form LAT - human
C;Species: Homo sapiens (man)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
C;Accession: A60764
R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 convert
A;Reference number: A60764; MUID:90007613; PMID:2571587
A;Accession: A60764
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: UNIPROT:Q8N4Y9
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin

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F;20-85/Domain: immunoglobulin homology <IMM>

  Query Match             53.0%;  Score 1628.5;  DB 2;  Length 377;
  Best Local Similarity   82.0%;  Pred. No. 1.9e-84;
  Matches  309;  Conservative   10;  Mismatches   11;  Indels   47;  Gaps    1;

Qy        120 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
              |||||||||||||| |:|||||||||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy        180 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV---------------------- 217
              |||||||||||||||||||| |||||||||||||:|
Db         61 GLYSLSSVVTVPSSSLGTQTYTCNVNHKPSNTKVDKRVELKTPLGDTTHTCPRCPEPKSC 120

Qy        218 ------------------------EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDT 252
                                       ||||||    || ||||||||||||||||||||||
Db        121 DTPPPCPRCPEPKSCDTPPPCPRCPEPKSCDTPPPCPRCPAPELLGGPSVFLFPPKPKDT 180

Qy        253 LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH 312
              ||||||||||||||||||||||:| ||||||||||||||||||||:||||||||||
Db        181 LMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQYNSTFRVVSVLTVLH 240

Qy        313 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK 372
              |||||||||||||||||||||||||| ||||||||||||||:|:||||||||||||
Db        241 QDWLNGKEYKCKVSNKALPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVK 300

Qy        373 GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE 432
              |||||||||||||:||||||| |||||||||||||||:|||||||||:||||||||||
Db        301 GFYPSDIAVEWESSGQPENNYNTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHE 360

Qy        433 ALHNHYTQKSLSLSPGK 449
              |||| :||||||||||
Db        361 ALHNRFTQKSLSLSPGK 377


RESULT 4
G2HU
Ig gamma-2 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 09-Jul-2004
C;Accession: A93906; A92809; A90752; A93132; A02148
R;Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
A;Reference number: A93906; MUID:82197621; PMID:6804948
A;Accession: A93906
A;Molecule type: DNA
A;Residues: 1-326 <ELL>
A;Cross-references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; P
A;Note: Lys-326 is probably removed posttranslationally
R;Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
A;Reference number: A92809; MUID:81007873; PMID:6774012
A;Contents: myeloma protein Til
A;Accession: A92809
A;Molecule type: protein
A;Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <WAN>
A;Note: Trp-156 is at or near the complement-binding site
R;Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A;Title: The amino acid sequences of the three heavy chain constant region domains of a
A;Reference number: A90752; MUID:80001357; PMID:113060
A;Contents: myeloma protein Zie
A;Accession: A90752
A;Molecule type: protein
A;Residues: 1-24,'E',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198-
A;Note: this sequence has since been revised
R;Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
A;Reference number: A93132; MUID:80114419; PMID:118920
A;Contents: Zie
A;Accession: A93132
A;Molecule type: protein
A;Residues: 238-275 <HOF>
R;Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A;Reference number: A94591
A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidat
ned
R;Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A;Reference number: A90253; MUID:72033500; PMID:4940472
A;Contents: annotation; myeloma protein Sa, disulfide bonds
R;Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A;Title: Structural studies of immunoglobulin G.
A;Reference number: A93157; MUID:69064124; PMID:5782707
A;Contents: annotation; Sa, disulfide bonds
C;Genetics:
A;Gene: GDB:IGHG2
A;Cross-references: GDB:119338; OMIM:147110
A;Map position: 14q32.33-14q32.33
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into l
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;133-202/Domain: immunoglobulin homology <IM2>
F;239-306/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83,140-200,246-304/Disulfide bonds: #status experimental
F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             52.2%;  Score 1604;  DB 1;  Length 326;
  Best Local Similarity   91.2%;  Pred. No. 3.7e-83;
  Matches  301;  Conservative   12;  Mismatches   13;  Indels    4;  Gaps    2;

Qy        120 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
              |||||||||||||| |:|||  ||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy        180 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 239
              |||||||||||||: ||||| |||:|||||||||| || | | :   |||||| : |
Db         61 GLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVE---CPPCPAPP-VAG 116

Qy        240 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299
              ||||||||||||||||||||||||||||||||||||:|||||||||||||||||||:|
Db        117 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFN 176

Qy        300 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359
              ||:||||||||:|||||||||||||| |||||||||| ||||||||||||||||||:|
Db        177 STFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREE 236

Qy        360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 419
              :||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db        237 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRW 296

Qy        420 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              ||||||||||||||||||||||||||||||
Db        297 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 326


RESULT 5
G4HU
Ig gamma-4 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
C;Accession: A90933; A90249; A02150
R;Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
```

```
A;Reference number: A90933; MUID:83157104; PMID:6299662
A;Accession: A90933
A;Molecule type: DNA
A;Residues: 1-327 <ELL>
A;Cross-references: UNIPROT:P01861
A;Note: the sequence was determined from the germline gene
R;Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A;Title: Human immunoglobulin sublclasses. Partial amino acid sequence of the constant r
A;Reference number: A90249; MUID:70207560; PMID:4192699
A;Accession: A90249
A;Molecule type: protein
A;Residues: 1-30;81-326 <PIN>
C;Genetics:
A;Gene: GDB:IGHG4
A;Cross-references: GDB:119340; OMIM:147130
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 111/1; 221/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;99-110/Region: hinge
F;134-203/Domain: immunoglobulin homology <IM2>
F;240-307/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83,141-201,247-305/Disulfide bonds: #status predicted
F;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;177/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             51.8%;  Score 1590.5;  DB 1;  Length 327;
  Best Local Similarity   90.9%;  Pred. No. 2.1e-82;
  Matches  300;  Conservative   12;  Mismatches   15;  Indels    3;  Gaps    1;

Qy        120 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
              ||||||||||||| |:|||  ||||||||||||||||||||||||||||||||||||||
Db          1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy        180 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 239
              ||||||||||||||||||:|| |||:||||||||||:|| |       || ||||| |||
Db         61 GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESK---YGPPCPSCPAPEFLGG 117

Qy        240 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299
              |||||||||||||||||||||||||||| |||||:|||||||||||||||||||||:|
Db        118 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFN 177

Qy        300 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359
              |||||||||||||||||||||||||||| ||: |||||||||||||||||||||::|
Db        178 STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEE 237

Qy        360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 419
              :|||||||||||||||||||||||||||||||||||||||||||||||:||||||||
Db        238 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRW 297

Qy        420 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |:||||||||||||||||||||||| ||
Db        298 QEGNVFSCSVMHEALHNHYTQKSLSLSLGK 327


RESULT 6
PC4436
monoclonal antibody 13-1 heavy chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C;Accession: PC4436
R;Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.
Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A;Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyr
A;Reference number: JC5810; MUID:98063277; PMID:9398605
A;Accession: PC4436
A;Molecule type: protein
A;Residues: 1-444 <AKA>
C;Comment: This catalytic antibody has peroxidase oxidase activity. It is directed again
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;251-320/Domain: immunoglobulin homology <IMM>
F;22/Disulfide bonds: interchain (to 98) #status predicted
F;99/Disulfide bonds: interchain (to 109) #status predicted

  Query Match             49.1%;  Score 1507.5;  DB 2;  Length 444;
  Best Local Similarity   60.9%;  Pred. No. 1.4e-77;
  Matches  276;  Conservative   74;  Mismatches   90;  Indels   13;  Gaps    6;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYIS--SGGSGT 58
              ||  ||:||  |:|| |||:||  ||| ||:| | |:|| | |||||:| |:  |   |
Db          1 EVQXVETGGGLVRPGNSLKLSCLTSGFTFSNYRMHWLRQPPGKRLEWIAVITVKSDNYGA 60

Qy         59 YYSDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVS 118
              |::||:||||||||::|:::||||  || ||:| |:| |      |  | |||||:: ||
Db         61 KYAESVRGRFTISRDDSKSSVYLQMNRLREEDTATYYCCRTP-WVYAMDCWGQGTSVIVS 119

Qy        119 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 178
              || |  |||:|||| | : :     |||||| ||||||||:||||:|:|||||||||||
Db        120 SAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQS 179

Qy        179 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP--CPAPEL 236
                ||:||| ||||||:  ::|  ||| |  |:||||||: |: |     | |  |  ||:
Db        180 D-LYTLSSSVTVPSSTWPSETVTCNVAHPASSTKVDKKIVPRDCG----CKPCICTVPEV 234

Qy        237 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 296
                  |||:||||||| | |: ||:||||||:| :||||:|:|:|| |||| |:|:||||
Db        235 ---SSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREE 291

Qy        297 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 356
              |:|||:| || | ::|||||||||:||:|:: | |||||||||| ||:|: ||||||:||
Db        292 QFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPP 351

Qy        357 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 416
              :::: |::||||||::  |:| || |||: |||| ||| | |::|:|||:|:|||| | |
Db        352 KEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNVQK 411

Qy        417 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              | |: || |:|||:|| ||||:|:|||| ||||
Db        412 SNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK 444


RESULT 7
S22080
Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine
N;Alternate names: Ig gamma-1 chain C region (clone 8.10)
C;Species: Bos primigenius taurus (cattle)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S22080; S06610; A31303
R;Sanders, P.G.
submitted to the EMBL Data Library, November 1991
A;Reference number: S22080
A;Accession: S22080
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-470 <SAN>
A;Cross-references: EMBL:X62916; NID:g439; PIDN:CAA44699.1; PID:g440
R;Symons, D.B.A.; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989
A;Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gam
A;Reference number: S06610; MUID:90097956; PMID:2513487
A;Accession: S06610
A;Molecule type: DNA
A;Residues: 142-470 <SYM>
A;Cross-references: EMBL:X16701
A;Note: the sequence was determined from the germline gene
C;Genetics:
A;Gene: Ig CH gamma-1
A;Introns: 98/1; 111/1; 221/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein
F;161-225/Domain: immunoglobulin homology <IMM>
```

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F;318/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match            47.7%;  Score 1466;  DB 2;  Length 470;
  Best Local Similarity  61.5%;  Pred. No. 3.3e-75;
  Matches  280;  Conservative   60;  Mismatches  105;  Indels   10;  Gaps    6;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              :| | |||   |||  :| ::|  |||: | ||::|||| | | |||| |:|||: |||
Db         20 QVQLRESGPSLVKPSQTLSLTCTVSGFSLSSYALTWVRQAPGKALEWVGGITSGGT-TYY 78

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTY----YFDSWGQGTTLT 116
              : ::| | :|:::|:|: : | : |:  ||:| |:| |    |         |:|||  :|
Db         79 NPALKSRLSITKENSKSQVSLSVSSVTPEDTATYYCARSTYGEVGDGAIADAWGQGLLVT 138

Qy        117 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 176
              ||||||  | |:||:      |  |  |||||  | |||||||:|||||| ||||||||||
Db        139 VSSASTTAPKVYPLSSCCGDKSSSTVTLGCLVSSYMPEPVTVTWNSGALKSGVHTFPAVL 198

Qy        177 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 236
              ||||||||||:|||| |: | ||: ||| |  |:|||| |:| :| |    |  || |||
Db        199 QSSGLYSLSSMVTVPGSTSG-QTFTCNVAHPASSTKVDKAVDP-TC-KPSPCDCCPPPEL 255

Qy        237 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 296
              ||||||:||||||||| || |||||||||| |:||||||:|:|| |||: | ||||||
Db        256 PGGPSVFIFPPKPKDTLTISGTPEVTCVVVDVGHDDPEVKFSWFVDDVEVNTATTKPREE 315

Qy        297 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 356
              |:||||||||| | : ||||  |||:|||| |: ||||| :|||: ||  |||||| | |
Db        316 QFNSTYRVVSALRIQHQDWTGGKEFKCKVHNEGLPAPIVRTISRTKGPAREPQVYVLAPP 375

Qy        357 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGSFFLYSKLTV 414
              ::||:|: |||||:|  |||  |||||: ||||   |: | |||| ||:| |:|||||  |
Db        376 QEELSKSTVSLTCMVTSFYPDYIAVEWQRNGQPESEDKYGTTPPQLDADSSYFLYSKLRV 435

Qy        415 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |:: ||:|: ::| |||||||||||||| | | ||
Db        436 DRNSWQEGDTYTCVVMHEALHNHYTQKSTSKSAGK 470


RESULT 8
S37483
Ig gamma-2a chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37483
R;Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A;Reference number: S37483
A;Accession: S37483
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-469 <DUC>
A;Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;276-345/Domain: immunoglobulin homology <IMM>

  Query Match            46.6%;  Score 1430.5;  DB 2;  Length 469;
  Best Local Similarity  58.8%;  Pred. No. 3.2e-73;
  Matches  266;  Conservative   71;  Mismatches  110;  Indels    5;  Gaps    4;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              :: | :|| : |||| |:|:|| |||: |: | ::||:| | : |:|: :|       | |
Db         20 QIQLQQSGPELVKPGASVKISCKASGYTFTDYYINWVKQKPGQGLKWIGWIYPASGNTKY 79

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGT-YYFDSWGQGTTLTVSS 119
              ::: ||: |:: | : :| |:|: || |||:|:||| |     |     | ||||||||||
Db         80 NENFKGKATLTVDTSSSTAYMQLSSLTSEDTAVYFCARAMGATATLLDYWGQGTTLTVSS 139

Qy        120 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
              | |  |||:|||    |:| :  |||||| |||||||::||||:|:||||||||||||
Db        140 AKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSD 199

Qy        180 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP--CPAPELL 237
              ||:||| ||| ||:  :|:  ||| |  |:|||||:||:       |||  |||| ||
Db        200 -LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRG-PTIKPCPPCKCPAPNLL 257

Qy        238 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297
              ||||||:|||| || |||| :| |||||||| :||:|: :|:|: |||| |:|:   |
Db        258 GGPSVFIFPPKIKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHRED 317

Qy        298 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 357
              |||| |||| | : ||||::|||:||||:|| ||||||:|||| ||  | |||| |||
Db        318 YNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPPE 377

Qy        358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 417
              :|:|| ||:|||:|  | | || ||| :||: | ||| | ||||||||:|:|||| |:|
Db        378 EEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKK 437

Qy        418 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              | : | :||||:|| ||||:| || | :|||
Db        438 NWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK 469


RESULT 9
S69339
Ig heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C;Accession: S69339; S72664
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A;Reference number: S69339; MUID:95262687; PMID:7744049
A;Accession: S69339
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <KHA>
A;Cross-references: EMBL:X81695
R;Khamlichi, A.A.
submitted to the EMBL Data Library, September 1994
A;Reference number: S72664
A;Accession: S72664
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140,'C',142-374 <KH2>
A;Cross-references: EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology

  Query Match            46.3%;  Score 1423;  DB 2;  Length 374;
  Best Local Similarity  61.9%;  Pred. No. 6.4e-73;
  Matches  281;  Conservative   23;  Mismatches   46;  Indels  104;  Gaps    4;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSH--YAMSWVRQTPAKRLEWVAYISSGGSGT 58
              ::|| |||   |||  :| ::|  |||: |     : |:|| | : |||:| |
Db         20 QITLKESGPTLVKPTQTLTLTCTFSGFSLSKSGVGVGWIRQPPGQALEWLALI-FWDDDK 78

Qy         59 YYSDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLG---TYYFDSWGQGTTL 115
                || |:: | ||::| :|| : | | ::   |:| |:|     |    | | |||||| :
Db         79 RYSPSLRTRLTITKDTSKNQVVLTMTNVDPADTATYYCGYSVEGYGQGYRFHSWGQGTLV 138

Qy        116 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 175
              ||||
Db        139 TVSS---------------------------------------------------------- 142

Qy        176 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE 235
                                                   ||||||||||||||||||
Db        143 ----------------------------------------EPKSCDKTHTCPPCPAPE 160

Qy        236 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 220

Qy        296 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 280
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Qy        356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 415
              ||:|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 340

Qy        416 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||||||||||||||||||
Db        341 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 374


RESULT 10
S40295
Ig gamma-2a chain (mAb735) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C;Accession: S40295
R;Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Bi
submitted to the EMBL Data Library, January 1993
A;Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against
A;Reference number: S40295
A;Accession: S40295
A;Molecule type: protein
A;Residues: 1-446 <KLE>
A;Cross-references: UNIPROT:Q99L25
C;Genetics:
A;Map position: 12
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid
F;1-446/Product: Ig gamma-2a chain #status experimental <MAT>
F;1-117/Domain: V-D-J region <VDJ>
F;118-446/Domain: C region <CHR>
F;118-214/Domain: C1 region <CH1>
F;215-230/Region: hinge
F;231-340/Domain: C2 region <CH2>
F;341-446/Domain: C3 region <CH3>
F;360-427/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted
F;132/Disulfide bonds: interchain (to light chain) #status predicted
F;224,227,229/Disulfide bonds: interchain #status predicted
F;297/Binding site: carbohydrate (Asn) (covalent) #status experimental

  Query Match             46.3%;  Score 1421;  DB 2;  Length 446;
  Best Local Similarity   58.7%;  Pred. No. 1e-72;
  Matches  264;  Conservative   71;  Mismatches  109;  Indels    6;  Gaps    4;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              :: | :|| : |:|| |:|:|| |||: |: | : ||:| | : |||: :|  |    | |
Db          1 QIQLQQSGPELVRPGASVKISCKASGYTFTDYYIHWVKQRPGEGLEWIGWIYPGSGNTKY 60

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSSA 120
              ::  ||: |:: | : :| |:|: || |||||:||| |    | :  | |||||::|||||
Db         61 NEKFKGKATLTVDTSSSTAYMQLSSLTSEDSAVYFCARG--GKFAMDYWGQGTSVTVSSA 118

Qy        121 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180
              |  |||:||||    |:| :  |||||| |||||||::||||:|:||||||||||||
Db        119 KTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSD- 177

Qy        181 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP--CPAPELLG 238
              ||:||| ||| ||:  :|:  ||| |  |:||||||:||:       |||  |||| |||
Db        178 LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRG-PTIKPCPPCKCPAPNLLG 236

Qy        239 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 298
              |||||:|||| || |||| :| ||||||||| :||:|: :|:|: |||  |:|:   | |
Db        237 GPSVFIFPPKIKDVLMISLSPMVTCVVVDVSEDDPDVQISWFVNNVEVLTAQTQTHREDY 296

Qy        299 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 358
              ||| |||| | : ||||::|||:||||:|| ||||||:|||| ||  | |||| |||  :
Db        297 NSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPPEE 356

Qy        359 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 418
              |:|| ||:|||:|  | | || ||| :||: | ||| | ||||||||:|:|||| |:|
Db        357 EMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKN 416

Qy        419 WQQGNVFSCSVMHEALHNHYTQKSLSLSPG 448
              | : | :||||:|| ||||:| || | :||
Db        417 WVERNSYSCSVVHEGLHNHHTTKSFSRTPG 446


RESULT 11
S31459
Ig gamma-1 chain - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C;Accession: S31459
R;Patri, S.; Nau, F.
submitted to the EMBL Data Library, December 1992
A;Reference number: S31459
A;Accession: S31459
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-472 <PAT>
A;Cross-references: EMBL:X69797
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;277-346/Domain: immunoglobulin homology <IMM>

  Query Match             46.0%;  Score 1412;  DB 2;  Length 472;
  Best Local Similarity   58.4%;  Pred. No. 3.5e-72;
  Matches  269;  Conservative   66;  Mismatches  108;  Indels   18;  Gaps    5;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSG--- 57
              :| | |||        :| |:|  |||: ::| : |||| | | |||:     ||||
Db         18 QVRLQESGPSLATLLQTLSVTCTISGFSLNNYGVDWVRQAPGKALEWL-----GGSGYDE 72

Qy         58 -TYYSDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYY------FDSWG 110
                 |:  :| | :|::| :|: : | : :: :||:|:|:| ||   : :      :| ||
Db         73 DIDYNPVLKSRLSITKDTSKSQVSLTLSTVTTEDTAVYYCARVDYDSSHAFAYASYDFWG 132

Qy        111 QGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 170
               |  ::| |||  | |:||      ||     |||||  | ||||||:||||||||||
Db        133 PGLLISVLSASTTPPKVYPLTSCCGDTSSSIVTLGCLVSSYMPEPVTVTWNSGALTSGVH 192

Qy        171 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP 230
              ||||:|||||||||||||:|: | ||:|||| |  |:|||||:|||   |    |
Db        193 TFPAILQSSGLYSLSSVVTVPASTSGAQTFICNVAHPASSTKVDKRVEPGCPDPCKHC-R 251

Qy        231 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 290
              || ||| ||||||:||||||||| || |||||||||||  :||||:|:|:|| |||  |:
Db        252 CPPPELPGGPSVFIFPPKPKDTLTISGTPEVTCVVVDVGQDDPEVQFSWFVDNVEVRTAR 311

Qy        291 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 350
              |||||||:|||:|||| | : ||||  |||:|||| |:|||||| :|||: ||| |||||
Db        312 TKPREEQFNSTFRVVSALPIQHQDWTGGKEFKCKVHNEALPAPIVRTISRTKGQAREPQV 371

Qy        351 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGSFFL 408
              | | | ::||:|: :|:|||| ||||  |||||: ||||  |: | ||   ||:|||:||
Db        372 YVLAPPQEELSKSTLSVTCLVTGFYPDYIAVEWQKNGQPESEDKYGTTTSQLDADGSYFL 431

Qy        409 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              ||:| |||: ||:|: ::| ||||||||||||||:|  |||
Db        432 YSRLRVDKNSWQEGDTYACVVMHEALHNHYTQKSISKPPGK 472


RESULT 12
G2MS11
Ig gamma-2b chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1980 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: S25057; A02157; A26235; A26232; A26233; A53598
R;Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
submitted to the EMBL Data Library, July 1992
A;Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific
A;Reference number: S25057
A;Accession: S25057
A;Status: preliminary
```

```
A;Molecule type: mRNA
A;Residues: 1-474 <FIS>
A;Cross-references: UNIPROT:P01866; EMBL:X67210; NID:g54826; PIDN:CAA47649.1; PID:g54827
R;Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
Nature 283, 786-789, 1980
A;Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from n
A;Reference number: A02157; MUID:80120716; PMID:6766534
A;Contents: a allele
A;Accession: A02157
A;Molecule type: DNA
A;Residues: 138-161,'L',163-189,'FP',193-474 <YAM>
A;Cross-references: GB:J00461
A;Note: the sequence was determined from the germline gene
R;Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.
Science 206, 1299-1303, 1979
A;Title: Structure of the constant and 3' untranslated regions of the murine gamma2b hea
A;Reference number: A26235; MUID:80081501; PMID:117548
A;Contents: MPC 11
A;Accession: A26235
A;Molecule type: mRNA
A;Residues: 138-172,'P',174-189,'FP',193-376,'T',378-474 <TU1>
A;Note: Lys-474 is probably removed posttranslationally
R;Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.
Science 206, 1303-1306, 1979
A;Title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglo
A;Reference number: A26232; MUID:80081502; PMID:117549
A;Accession: A26232
A;Molecule type: DNA
A;Residues: 138-172,'P',174-189,'FP',193-376,'T',378-474 <TU2>
R;Ollo, R.; Rougeon, F.
Nature 296, 761-763, 1982
A;Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamm
A;Reference number: A26233; MUID:82173203; PMID:6803173
A;Contents: b allele
A;Accession: A26233
A;Molecule type: DNA
A;Residues: 138-161,'L',163-189,'FP',193-300,'R',302-331,'A',333-437,'DI',440-474 <OLL>
A;Cross-references: GB:J00461
R;Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahash
J. Biol. Chem. 269, 12345-12350, 1994
A;Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.
A;Reference number: A53598; MUID:94216359; PMID:7512967
A;Accession: A53598
A;Status: preliminary
A;Molecule type: protein
A;Residues: 234-251 <KIM>
C;Comment: The a allele sequence is shown.
C;Genetics:
A;Introns: 138/1; 236/1; 258/1; 368/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobu
F;157-222/Domain: immunoglobulin homology <IM1>
F;236-257/Region: hinge
F;281-350/Domain: immunoglobulin homology <IM2>
F;387-454/Domain: immunoglobulin homology <IM3>
F;152/Disulfide bonds: interchain (to light chain) #status predicted
F;164-220,288-348,394-452/Disulfide bonds: #status predicted
F;247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicted
F;324/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             44.4%;  Score 1365;  DB 1;  Length 474;
  Best Local Similarity   55.8%;  Pred. No. 1.6e-69;
  Matches  256;  Conservative   72;  Mismatches  117;  Indels   14;  Gaps    4;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || | :|| : | || |:|:|| |||: |  | | ||:| | : |||: ||:    || :
Db         20 EVQLQQSGPELVNPGASVKMSCKASGYTFITYVMHWVKQKPGQGLEWIGYINPNKDGTKF 79

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTY---YFDSWGQGTTLTV 117
                ::  ||: |:: | : || |::: || |||||:|:| |     |   :|  ||||| :||
Db         80 NEKFKGKATLTSDKSSNTAYMELSSLTSEDSAVYYCAR----DYDYDWFAYWGQGTLVTV 135

Qy        118 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 177
              |:| |  |||:||||    |:| :  ||||| |||| |||:||||:|:| |||    |
Db        136 SAAKTTPPSVYPLAPGCGDTTGSSVTSGCLVKGYFPESVTVTWNSGSLSSSVHTLSQALL 195

Qy        178 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT-HTCPP------ 230
              ||||::|| ||||||:  :||  |:| |  |:| ||||:||     | : |||
Db        196 QSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECHK 255

Qy        231 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 290
              |||| | ||||||:|||  || |||| ||:|||||||| :||:|: :|:|: |||| |:
Db        256 CPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQ 315

Qy        291 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 350
              |:   | |||| |||| | : ||||::|||:||||:|| ||:|||:|||| ||  | |||
Db        316 TQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQV 375

Qy        351 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 410
              | |||  ::|::  ||||||| || | ||:||| |||  | ||| | |||||||:|:||
Db        376 YILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYS 435

Qy        411 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              || :  |:|:: : |||:| || | |:| :|::| ||||
Db        436 KLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 474


RESULT 13
S01321
Ig gamma-2b chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
C;Accession: S01321
R;de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
Eur. J. Biochem. 176, 287-295, 1988
A;Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed
A;Reference number: S01320; MUID:88329081; PMID:3138116
A;Accession: S01321
A;Molecule type: mRNA
A;Residues: 1-475 <DE1>
A;Cross-references: EMBL:X13188; NID:g51780; PIDN:CAA31580.1; PID:g51781
A;Note: this sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-475/Product: Ig gamma-2b chain #status predicted <MAT>
F;159-223/Domain: immunoglobulin homology <IMM>

  Query Match             43.7%;  Score 1343.5;  DB 2;  Length 475;
  Best Local Similarity   55.4%;  Pred. No. 2.5e-68;
  Matches  253;  Conservative   75;  Mismatches  120;  Indels    9;  Gaps    4;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              :| | :|| :  :|| |:|:|| |||:  : | :|||:|   : |||:  |  |   :|:
Db         20 QVQLQQSGAELARPGASVKLSCKASGYTLTSYGISWVKQRTGQGLEWIGEIYPGSGNSYF 79

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVK-LGTYYFDSWGQGTTLTVSS 119
              ::  ||: |:: | : :| || : || |||||:|||   : :|   | |||||:| |:
Db         80 NEKFKGKATLTVDKSSSTAYLHLSSLTSEDSAVYFCAGPRQVGLLPFGYWGQGTLVTASA 139

Qy        120 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
              | |  |||:||||    |:| :  |||||| |||| |||:||||:|:| ||||||:|| |
Db        140 AKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQ-S 198

Qy        180 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT-HTCPP------CP 232
              |||::|| ||||||:  :||  |:| |  |:| ||||:||     | : |||      ||
Db        199 GLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPTSTINPCPPCKECHKCP 258

Qy        233 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 292
              || | ||||||:|||  || |||| ||:|||||||| :||:|: :|:|: |||  |:|:
Db        259 APNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVLTAQTQ 318

Qy        293 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT 352
                | |||| |||| | : ||||::|||:||||:|| ||||||:|||| ||  | ||||
```

```
Db        319 THREDYNSTIRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKIKGIVRAPQVYI 378

Qy        353 LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL 412
              | |  ::|::  |||||  || | ||:||| |||  | ||| | ||||||||:|:|||| 
Db        379 LSPPPEQLSRKDVSLTCLAVGFSPEDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKL 438

Qy        413 TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
               :  |:|:: : |||:| || | |:| :|::| ||||
Db        439 NMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 475


RESULT 14
I47159
Ig gamma 2a chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47159
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47159
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124
C;Genetics:
A;Gene: IgG2a
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>

  Query Match             41.1%;  Score 1263;  DB 2;  Length 328;
  Best Local Similarity   69.6%;  Pred. No. 5.3e-64;
  Matches  231;  Conservative   43;  Mismatches   52;  Indels    6;  Gaps    2;

Qy        120 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
              |    |||:|||| |: |||   |||||   ||||||||:||||||:|||||||:||| |
Db          1 APKTAPSVYPLAPCSRDTSGPNVALGCLASSYFPEPVTVTWNSGALSSGVHTFPSVLQPS 60

Qy        180 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 239
              |||||||:||||:||| :::| |||||  : |||||:|  |:       || | :|    |
Db         61 GLYSLSSMVTVPASSLSSKSYTCNVNHPATTTKVDKRVGTKTKPPCPICPACESP----G 116

Qy        240 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299
              ||||:|||||||||||||:|||||||| |:|||:|:|||||||| |:|:|:|:||:|
Db        117 PSVFIFPPKPKDTLMISRTPQVTCVVVDVSQENPEVQFSWYVDGVEVHTAQTRPKEEQFN 176

Qy        300 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 359
              ||||||||| : |||||||:||||:|| ||||| : ||||||| |||||||||  :|
Db        177 STYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAKGQTREPQVYTLPPHAEE 236

Qy        360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGSFFLYSKLTVDKS 417
              |:::||:|||| |||| || |||: |||  || ||:|||  | ||::||||| :|||:
Db        237 LSRSKVSITCLVIGFYPPDIDVEWQRNGQPEPEGNYRTTPPQQDVDGTYFLYSKFSVDKA 296

Qy        418 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
               || | :| |:|||||||||||||:| :|||
Db        297 SWQGGGIFQCAVMHEALHNHYTQKSISKTPGK 328


RESULT 15
S31866
Ig gamma-1 chain C region - synthetic
C;Species: synthetic
A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C;Accession: S31866
R;Filpula, D.
submitted to the EMBL Data Library, February 1993
A;Description: Screeing method for protein-protein interactions of cloned gene products.
A;Reference number: S31866
A;Accession: S31866
A;Molecule type: mRNA
A;Residues: 1-255 <FIL>
A;Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
C;Keywords: immunoglobulin
F;1-22/Region: Escherichia coli outer membrane protein A precursor
F;23-255/Region: human Ig gamma-1 chain C region

  Query Match             41.0%;  Score 1260;  DB 4;  Length 255;
  Best Local Similarity   97.5%;  Pred. No. 5.8e-64;
  Matches  233;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy        211 TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH 270
              |     || ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 TVAQADVESKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH 76

Qy        271 EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL 330
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL 136

Qy        331 PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE 390
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE 196

Qy        391 NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 255


Search completed: December 23, 2004, 19:06:08
Job time : 33.449 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2004, 18:31:20 ; Search time 161.904 Seconds
(without alignments)
2068.313 Million cell updates/sec

Title: US-10-089-500-57
Perfect score: 3071
Sequence: 1 EVTLVESGGDFVKPGGSLKV.....IVEFLNRWITFCQSIISTLT 582

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2195.5	71.5	471	2	AAH24289	Aah24289 homo sapi
2	2184	71.1	470	2	Q6PJA4	Q6pja4 homo sapien
3	2184	71.1	470	2	AAH18747	Aah18747 homo sapi
4	2184	71.1	478	2	Q6PI81	Q6pi81 homo sapien
5	2184	71.1	478	2	AAH41037	Aah41037 homo sapi
6	2166.5	70.5	475	2	Q6MZQ6	Q6mzq6 homo sapien
7	2166.5	70.5	475	2	CAE45972	Cae45972 homo sapi
8	2166	70.5	472	2	BAC85232	Bac85232 homo sapi
9	2160	70.3	472	2	Q6N089	Q6n089 homo sapien
10	2160	70.3	472	2	CAE45781	Cae45781 homo sapi
11	2157.5	70.3	475	2	Q6GMW7	Q6gmw7 homo sapien
12	2154.5	70.2	479	2	AAH06402	Aah06402 homo sapi
13	2152.5	70.1	473	2	Q6MZV7	Q6mzv7 homo sapien
14	2152.5	70.1	473	2	CAE45920	Cae45920 homo sapi
15	2148	69.9	468	2	BAC85444	Bac85444 homo sapi
16	2146	69.9	480	2	Q6N094	Q6n094 homo sapien
17	2146	69.9	480	2	CAE45776	Cae45776 homo sapi
18	2145	69.8	466	2	Q6IN78	Q6in78 homo sapien
19	2140.5	69.7	544	2	Q6PJ95	Q6pj95 homo sapien
20	2140.5	69.7	544	2	AAH19046	Aah19046 homo sapi
21	2126	69.2	466	2	Q6N096	Q6n096 homo sapien
22	2126	69.2	466	2	CAE45774	Cae45774 homo sapi
23	2124.5	69.2	473	2	Q6P055	Q6p055 homo sapien
24	2124.5	69.2	473	2	AAH65820	Aah65820 homo sapi
25	2124	69.2	470	2	Q7Z5W1	Q7z5w1 homo sapien
26	2123	69.1	478	2	BAC85385	Bac85385 homo sapi
27	2122	69.1	464	2	BAC85373	Bac85373 homo sapi
28	2120.5	69.0	471	2	BAC85388	Bac85388 homo sapi
29	2113	68.8	466	2	AAH64496	Aah64496 homo sapi
30	2111	68.7	482	2	Q7Z351	Q7z351 homo sapien
31	2105	68.5	470	2	BAC85172	Bac85172 homo sapi
32	2103	68.5	474	2	BAC85350	Bac85350 homo sapi
33	2095.5	68.2	479	2	AAH14667	Aah14667 homo sapi
34	2090	68.1	464	2	AAH19337	Aah19337 homo sapi
35	2088	68.0	468	2	BAC85175	Bac85175 homo sapi
36	2083	67.8	474	2	BAC85171	Bac85171 homo sapi
37	2080.5	67.7	481	2	Q6N097	Q6n097 homo sapien
38	2080.5	67.7	481	2	CAE45773	Cae45773 homo sapi
39	2066.5	67.3	469	2	Q7Z7P5	Q7z7p5 homo sapien
40	2057	67.0	470	2	AAH62336	Aah62336 homo sapi
41	2055	66.9	476	2	BAC05017	Bac05017 homo sapi
42	2054	66.9	472	2	BAC86225	Bac86225 homo sapi
43	2052.5	66.8	475	2	Q6N095	Q6n095 homo sapien
44	2052.5	66.8	475	2	CAE45775	Cae45775 homo sapi
45	2051	66.8	474	2	BAC05012	Bac05012 homo sapi

ALIGNMENTS

RESULT 1
AAH24289
ID AAH24289 PRELIMINARY; PRT; 471 AA.
AC AAH24289;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC024289; AAH24289.1; -.
KW Hypothetical protein.
SQ SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;

Query Match 71.5%; Score 2195.5; DB 2; Length 471;
Best Local Similarity 91.6%; Pred. No. 9.5e-133;
Matches 414; Conservative 16; Mismatches 19; Indels 3; Gaps 2;

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Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||  |||||||::||||||| || |:|:|||| | | ||||: :||  |  ||
Db         20 EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSMSSSSSYIYY 79

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTR--VKLGTY-YFDSWGQGTTLTV 117
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           :||||||||||||||||:||||| |||:||:|:|:| |   :| :| ||| ||:|| :||
Db         80 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDLRQLTSYWYFDLWGRGTLVTV 139

Qy        118 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 199

Qy        178 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 259

Qy        238 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 319

Qy        298 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 379

Qy        358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 439

Qy        418 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              ||||||||||||||||||||||||||||||||
Db        440 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 471
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RESULT 2
Q6PJA4
ID Q6PJA4 PRELIMINARY; PRT; 470 AA.
AC Q6PJA4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC018747; AAH18747.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF00047; ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51715 MW; 7B49556A11FD7D99 CRC64;

Query Match 71.1%; Score 2184; DB 2; Length 470;
Best Local Similarity 91.4%; Pred. No. 5.2e-132;
Matches 412; Conservative 10; Mismatches 27; Indels 2; Gaps 1;

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Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || |||||  |:|||||::||  ||| || | |||||| | | ||||| |   ||  ||
Db         20 EVQLVESGGGLVQPGGSLRLSCVVSGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYY 79

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTY--YFDSWGQGTTLTVS 118
               ||||||||||||||:||||| |||:||:|:|:| |     |  :|| ||||| :|||
Db         80 VDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDGSSWYRDWFDPWGQGTLVTVS 139

Qy        119 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 199

Qy        179 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 259

Qy        239 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 319

Qy        299 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 379

Qy        359 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 418
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 439

Qy        419 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              ||||||||||||||||||||||||||||||
Db        440 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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RESULT 3
AAH18747
ID AAH18747 PRELIMINARY; PRT; 470 AA.
AC AAH18747;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

```
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC018747; AAH18747.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   470 AA;  51715 MW;  7B49556A11FD7D99 CRC64;

  Query Match             71.1%;  Score 2184;  DB 2;  Length 470;
  Best Local Similarity   91.4%;  Pred. No. 5.2e-132;
  Matches  412;  Conservative   10;  Mismatches   27;  Indels    2;  Gaps    1;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
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Db         20 EVQLVESGGGLVQPGGSLRLSCVVSGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYY 79

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTY--YFDSWGQGTTLTVS 118
               |||||||||||||||:||||| |||:||:|:|:| |      |  :|| ||||| :|||
Db         80 VDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDGSSWYRDWFDPWGQGTLVTVS 139

Qy        119 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 178
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Db        140 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 199

Qy        179 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 238
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Db        200 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 259

Qy        239 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 298
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Db        260 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 319

Qy        299 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 379

Qy        359 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 418
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 439

Qy        419 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||||||||||||||||
Db        440 WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470


RESULT 4
Q6PI81
ID   Q6PI81      PRELIMINARY;      PRT;   478 AA.
AC   Q6PI81;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC041037; AAH41037.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   478 AA;  52666 MW;  17BED38D917970D6 CRC64;

  Query Match             71.1%;  Score 2184;  DB 2;  Length 478;
  Best Local Similarity   90.0%;  Pred. No. 5.3e-132;
  Matches  413;  Conservative   13;  Mismatches   23;  Indels   10;  Gaps    2;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||  |:||||::|||||| || | |||||| | | ||||| |   ||  ||
Db         20 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYY 79

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTR--------VKLGTYYF--DSWG 110
               |||||||||||||||:||||| |||:||:|:|:| |         |    |||  | ||
Db         80 VDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREFESTMTTVNADYYYFYMDVWG 139

Qy        111 QGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 170
              :|||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 KGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 199

Qy        171 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP 230
              ||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db        200 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPP 259

Qy        231 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 319

Qy        291 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 350
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 379

Qy        351 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 410
              |||||||:|:||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 439
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Qy        411 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||||||||||||||||||||||||
Db        440 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
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RESULT 5
AAH41037
ID AAH41037 PRELIMINARY; PRT; 478 AA.
AC AAH41037;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC041037; AAH41037.1; -.
KW Hypothetical protein.
SQ SEQUENCE 478 AA; 52666 MW; 17BED38D917970D6 CRC64;

Query Match 71.1%; Score 2184; DB 2; Length 478;
Best Local Similarity 90.0%; Pred. No. 5.3e-132;
Matches 413; Conservative 13; Mismatches 23; Indels 10; Gaps 2;

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Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || |||||  |:|||||::|||||| || | |||||| | | ||||| |   ||  ||
Db         20 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYY 79

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTR--------VKLGTYYF--DSWG 110
               |||||||||||||||:||||| |||:||:|:|:| |         |    |||  | ||
Db         80 VDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREFESTMTTVNADYYYFYMDVWG 139

Qy        111 QGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 170
              :|||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 KGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 199

Qy        171 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP 230
              |||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db        200 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPP 259

Qy        231 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        260 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 319

Qy        291 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 350
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 379

Qy        351 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 410
              |||||||:|:|||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 439

Qy        411 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||||||||||||||||||||||||
Db        440 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
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RESULT 6
Q6MZQ6
ID Q6MZQ6 PRELIMINARY; PRT; 475 AA.
AC Q6MZQ6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686G11190.
GN Name=DKFZp686G11190;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG THE GERMAN HUMAN CDNA CONSORTIUM;
RA Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BX640947; CAE45972.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF00047; ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8E CRC64;

Query Match 70.5%; Score 2166.5; DB 2; Length 475;
Best Local Similarity 89.0%; Pred. No. 7e-131;
Matches 406; Conservative 18; Mismatches 25; Indels 7; Gaps 1;

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Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || |:||||  |:|||||::||||||| | :|||:|||| | | ||||: ||| |  |||
Db         20 EVQLLESGGGLVQPGGSLRLSCAASGFTFRNYAMNWVRQAPGKGLEWVSGISSSGVNTYY 79

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTY-------YFDSWGQGT 113
              :||||||||| | : ||||||| |||::|:|:|:| |   |       ||| ||:||
Db         80 ADSVKGRFTISGDISTNTLYLQMHSLRADDTAVYYCARADYRDYQVSPAYWYFDVWGRGT 139

Qy        114 TLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 173
               ::||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 LVSVSAASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 199

Qy        174 AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA 233
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA 259

Qy        234 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 293
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        260 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 319

Qy        294 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 379

Qy        354 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 413
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 439

Qy        414 VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||| ||||||||||||||||
Db        440 VDKSRWQQGNVFSCSVMHEGLHNHYTQKSLSLSPGK 475


RESULT 7
CAE45972
ID   CAE45972    PRELIMINARY;      PRT;   475 AA.
AC   CAE45972;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein DKFZp686G11190.
GN   DKFZP686G11190.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Human esophagus tumor;
RA   Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA   Han M., Wiemann S.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX640947; CAE45972.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   475 AA;  52043 MW;  B7EAE255A26F4B8E CRC64;

  Query Match             70.5%;  Score 2166.5;  DB 2;  Length 475;
  Best Local Similarity   89.0%;  Pred. No. 7e-131;
  Matches  406;  Conservative   18;  Mismatches   25;  Indels    7;  Gaps    1;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || |:|||  |:|||||::|||||| | :|||:|||| | | |||||: ||| |  |||
Db         20 EVQLLESGGGLVQPGGSLRLSCAASGFTFRNYAMNWVRQAPGKGLEWVSGISSSGVNTYY 79

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTY-------YFDSWGQGT 113
              :|||||||||| | : ||||||| |||::|:|:|:| |       |       ||| ||:||
Db         80 ADSVKGRFTISGDISTNTLYLQMHSLRADDTAVYYCARADYRDYQVSPAYWYFDVWGRGT 139

Qy        114 TLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 173
               ::||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 LVSVSAASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 199

Qy        174 AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA 259

Qy        234 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 319

Qy        294 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 379

Qy        354 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 413
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 439

Qy        414 VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||| ||||||||||||||||
Db        440 VDKSRWQQGNVFSCSVMHEGLHNHYTQKSLSLSPGK 475


RESULT 8
BAC85232
ID   BAC85232    PRELIMINARY;      PRT;   472 AA.
AC   BAC85232;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   CDNA FLJ26265 fis, clone DMC05516, highly similar to Ig gamma-1 chain
DE   C region.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Dermoid tumor;
RA   Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y.,
RA   Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
RA   Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
RA   Kawakami B., Nagai K., Isogai T., Sugano S.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK129776; BAC85232.1; -.
SQ   SEQUENCE   472 AA;  51212 MW;  01BF215F99809164 CRC64;

  Query Match             70.5%;  Score 2166;  DB 2;  Length 472;
  Best Local Similarity   89.2%;  Pred. No. 7.5e-131;
  Matches  406;  Conservative   18;  Mismatches   23;  Indels    8;  Gaps    2;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || |:|||  |:|||||::|||||||   ||:|||| | | ||||: |   |  |||
Db         20 EVNLLQSGGGLVQPGGSLRLSCAASGFAFGGTAMTWVRQVPGKGLEWVSAIGGSGYSTYY 79

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYY------FDSWGQGTT 114
              :||| ||||:|||||: ||:|||| ||| ||:|||:| : ::|  |      ||:|||||
Db         80 ADSVTGRFTVSRDNSNNTVYLQMNSLRVEDTAMYYCAKDRVG--YGGNPDSFDAWGQGTM 137

Qy        115 LTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 174
              :|| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 VTVGSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 197

Qy        175 VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP 234
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP 257

Qy        235 ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 294
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 317

Qy        295 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP 354
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP 377

Qy        355 PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV 437

Qy        415 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||| ||||||||||||||||
Db        438 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 472


RESULT 9
Q6N089
ID   Q6N089      PRELIMINARY;      PRT;   472 AA.
AC   Q6N089;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein DKFZp686P15220.
GN   Name=DKFZp686P15220;
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OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Human rectum tumor;
RG   THE GERMAN HUMAN CDNA CONSORTIUM;
RA   Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX640627; CAE45781.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   472 AA;  51724 MW;  26CB340D0046D279 CRC64;

  Query Match             70.3%;  Score 2160;  DB 2;  Length 472;
  Best Local Similarity   89.9%;  Pred. No. 1.8e-130;
  Matches  408;  Conservative   16;  Mismatches   24;  Indels    6;  Gaps    3;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||  |:|| ||::||||||| |  ||| |||| | | ||||: ||       |
Db         20 EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIAY 79

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGT---YYF--DSWGQGTTL 115
              :|||||||||||||| ||:||||| |||:||:|:|:| : ::|    ||:  | ||||||:
Db         80 ADSVKGRFTISRDNGKNSLYLQMNSLRAEDTALYYCAK-EIGAHNFYYYGMDVWGQGTTV 138

Qy        116 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 198

Qy        176 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE 235
              ||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||
Db        199 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPE 258

Qy        236 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 318

Qy        296 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 378

Qy        356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 415
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 438

Qy        416 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||||||||||||||||||
Db        439 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 472


RESULT 10
CAE45781
ID   CAE45781    PRELIMINARY;      PRT;   472 AA.
AC   CAE45781;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein DKFZp686P15220.
GN   DKFZP686P15220.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Human rectum tumor;
RA   Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX640627; CAE45781.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   472 AA;  51724 MW;  26CB340D0046D279 CRC64;

  Query Match             70.3%;  Score 2160;  DB 2;  Length 472;
  Best Local Similarity   89.9%;  Pred. No. 1.8e-130;
  Matches  408;  Conservative   16;  Mismatches   24;  Indels    6;  Gaps    3;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||  |:|| ||::||||||| |  ||| |||| | | ||||: ||       |
Db         20 EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIAY 79

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGT---YYF--DSWGQGTTL 115
              :|||||||||||||| ||:||||| |||:||:|:|:| : ::|    ||:  | ||||||:
Db         80 ADSVKGRFTISRDNGKNSLYLQMNSLRAEDTALYYCAK-EIGAHNFYYYGMDVWGQGTTV 138

Qy        116 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 198

Qy        176 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE 235
              ||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||
Db        199 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPE 258

Qy        236 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 318

Qy        296 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 378

Qy        356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 415
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 438

Qy        416 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||||||||||||||||||
Db        439 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 472


RESULT 11
Q6GMW7
ID   Q6GMW7      PRELIMINARY;      PRT;   475 AA.
AC   Q6GMW7;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073782; AAH73782.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   475 AA;  51987 MW;  2A1FE55D736860F8 CRC64;

  Query Match           70.3%;  Score 2157.5;  DB 2;  Length 475;
  Best Local Similarity  89.5%;  Pred. No. 2.6e-130;
  Matches  408;  Conservative   15;  Mismatches   26;  Indels    7;  Gaps    2;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||  |:|||||::|| || |  | :|| |||| | | ||:|: ||:  : |||
Db         20 EVQLVESGGGLVQPGGSLRLSCVASAFTLSRHAMHWVRQAPGKGLEYVSGISNSENSTYY 79

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVK------LGTYY-FDSWGQGT 113
              :|||||||||||||| |||||||: |||:|| |:|:| | :      |  ||  | |||||
Db         80 ADSVKGRFTISRDNYKNTLYLQLGSLRAEDKAVYYCARARCRGDTCLNFYYGLDVWGQGT 139

Qy        114 TLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 173
              |: |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 TVIVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 199

Qy        174 AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA 259

Qy        234 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 319

Qy        294 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 379

Qy        354 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 413
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 439

Qy        414 VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              ||||||||||||||||||||||||||||||||||||
Db        440 VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 475


RESULT 12
AAH06402
ID   AAH06402    PRELIMINARY;      PRT;   479 AA.
AC   AAH06402;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC006402; AAH06402.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   479 AA;  52281 MW;  D74E0C89082A9788 CRC64;

  Query Match           70.2%;  Score 2154.5;  DB 2;  Length 479;
  Best Local Similarity  88.7%;  Pred. No. 4.2e-130;
  Matches  408;  Conservative   15;  Mismatches   26;  Indels   11;  Gaps    2;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              || ||||||  |:|| ||::|||||| | ||| |||| | | ||||: ||       |
Db         20 EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQVPGKGLEWVSGISCNSGSIGY 79

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTR-VKL----------GTYYFDSW 109
              :|||||||||||||| :||||| |||:||:|:|:| : ::|          |:  || |
Db         80 ADSVKGRFTISRDNAKKSLYLQMNSLRAEDTALYYCAKDIELDIVVVPAPMRGSLGFDYW 139

Qy        110 GQGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV 169
              |||| :|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 GQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV 199

Qy        170 HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP 229
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP 259

Qy        230 PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 289
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 319

Qy        290 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 379

Qy        350 VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY 409
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY 439

Qy        410 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
                 |||||||||||||||||||||||||||||||||||||||
Db        440 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 479


RESULT 13
Q6MZV7
ID   Q6MZV7      PRELIMINARY;      PRT;   473 AA.
AC   Q6MZV7;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein DKFZp686C11235.
GN   Name=DKFZp686C11235;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Human small intestine;
RG   THE GERMAN HUMAN CDNA CONSORTIUM;
RA   Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX640853; CAE45920.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   473 AA;  52121 MW;  9476EAE4C0BFC447 CRC64;

  Query Match             70.1%;  Score 2152.5;  DB 2;  Length 473;
  Best Local Similarity   88.3%;  Pred. No. 5.5e-130;
  Matches  401;  Conservative   24;  Mismatches   24;  Indels    5;  Gaps    1;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              |: ||||||  |:|||||::|||||||  || : |:|||| | | |||::||:  |:  ||
Db         20 EIQLVESGGGLVQPGGSLRLSCAASGFTFSSFEMNWVRQAPGKGLEWLSYITRSGNTVYY 79

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGT-----YYFDSWGQGTTL 115
              :||::||||||||||:|:||||| |||:||:|:|:| |    |       :|| ||||  :
Db         80 ADSLQGRFTISRDNARNSLYLQMNSLRAEDTAVYYCARQNEHTSPWYPSFFDYWGQGILV 139

Qy        116 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 175
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        140 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFLEPVTVSWNSGALTSGVHTFPAV 199

Qy        176 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE 235
              ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db        200 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPE 259

Qy        236 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 319

Qy        296 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 379

Qy        356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 415
              ||:|:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 439

Qy        416 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||||||||||||||||||||
Db        440 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 473


RESULT 14
CAE45920
ID   CAE45920    PRELIMINARY;      PRT;   473 AA.
AC   CAE45920;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein DKFZp686C11235.
GN   DKFZP686C11235.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Human small intestine;
RA   Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX640853; CAE45920.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   473 AA;  52121 MW;  9476EAE4C0BFC447 CRC64;

  Query Match             70.1%;  Score 2152.5;  DB 2;  Length 473;
  Best Local Similarity   88.3%;  Pred. No. 5.5e-130;
  Matches  401;  Conservative   24;  Mismatches   24;  Indels    5;  Gaps    1;

Qy          1 EVTLVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYY 60
              |: ||||||  |:|||||::|||||||  || : |:|||| | | |||::||:  |:  ||
Db         20 EIQLVESGGGLVQPGGSLRLSCAASGFTFSSFEMNWVRQAPGKGLEWLSYITRSGNTVYY 79

Qy         61 SDSVKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGT-----YYFDSWGQGTTL 115
              :||::||||||||||:|:||||| |||:||:|:|:| |    |       :|| ||||  :
Db         80 ADSLQGRFTISRDNARNSLYLQMNSLRAEDTAVYYCARQNEHTSPWYPSFFDYWGQGILV 139

Qy        116 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 175
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        140 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFLEPVTVSWNSGALTSGVHTFPAV 199

Qy        176 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE 235
              ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db        200 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPE 259

Qy        236 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 319

Qy        296 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 379

Qy        356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 415
              ||:|:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 439

Qy        416 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||||||||||||||||||||
Db        440 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 473


RESULT 15
BAC85444
ID   BAC85444    PRELIMINARY;      PRT;   468 AA.
AC   BAC85444;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
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DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   CDNA FLJ27334 fis, clone TMS09201, highly similar to Ig gamma-1 chain
DE   C region.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Thymus;
RA   Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H.,
RA   Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
RA   Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T.,
RA   Sugano S.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK130844; BAC85444.1; -.
SQ   SEQUENCE   468 AA;  51224 MW;  9280ACAD6817FC20 CRC64;

  Query Match             69.9%;  Score 2148;  DB 2;  Length 468;
  Best Local Similarity   89.7%;  Pred. No. 1.1e-129;
  Matches  400;  Conservative   18;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          4 LVESGGDFVKPGGSLKVSCAASGFAFSHYAMSWVRQTPAKRLEWVAYISSGGSGTYYSDS 63
              ||||||  ||| |||::||:|||| || | | | || | | |||::|||  |    |:::|
Db         23 LVESGGGLVKPEGSLRLSCSASGFTFSDYYMGWTRQAPGKGLEWISYISDSGLSQYHAES 82

Qy         64 VKGRFTISRDNAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYFDSWGQGTTLTVSSASTK 123
              ||||||:|||||||:| |||  ||:||:|:|:| |: :     : ||||| :|||||||
Db         83 VKGRFTVSRDNAKNSLSLQMNRLRAEDTAVYYCARLVVRGVIINLWGQGTLVTVSSASTK 142

Qy        124 GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS 202

Qy        184 LSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVF 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 LSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVF 262

Qy        244 LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR 322

Qy        304 VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKN 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKN 382

Qy        364 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN 442

Qy        424 VFSCSVMHEALHNHYTQKSLSLSPGK 449
              |||||||||||||||||||||||||
Db        443 VFSCSVMHEALHNHYTQKSLSLSPGK 468


Search completed: December 23, 2004, 19:04:41
Job time : 162.904 secs
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